STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 204048

TO: Ruixiang Li
Location: rem/4D75/4C70
Art Unit: 1646
Friday, October 13, 2006
Case Serial Number: 10/668767

From: Dwayne Hill
Location: Biotech-Chem Library
REM-1A41
Phone: (571)272-8972

Dwayne.Hill@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Dwayne Hill
STIC Biotech/Chem Library
(571)272-1972

78733

10-324

204048

1114

STIC-Biotech/ChemLib

From: Li, Ruixiang
Sent: CRFF Friday, October 06, 2006 11:40 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/668,767

Please do a standard search on: aa 5128

(i). SEQ ID NO: 128 against interference amino acid databases;

(ii). SEQ ID NO: 127 and ~~128~~ against interference nucleic acid databases.

Thank you very much!

127 na 15387

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

Seq ID 127 1-5000

Em ☐
Log ☐

MEq

****
Searcher: 10/4
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

****
Type of Search
NA# AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

Li, Ruixiang

From: Hill, Dwayne (ASRC)
Sent: Tuesday, October 24, 2006 1:52 PM
To: Li, Ruixiang
Subject: Sequence Search Results for 10/668767 Seq. ID 128 (1-1700)

Dear Examiner,

I just checked SCORE and the results for your sequence search are there now.

****

http://es/ScoreAccessWeb/GetItems.action?AppId=10668767&ItemType=4&VersionNo=10

After downloading files, use Microsoft Word to view, manipulate and print.

****

If you have any problems, please do not hesitate to call me for assistance.

Please let me know if you have any questions. Thank you for using STIC services.

Dwayne Hill
STIC/Biotech Library
REM1A64
X28972

search
:dback form.d

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 6, 2006, 23:32:44 ; Search time 87 Seconds
(without alignments)
5159.277 Million cell updates/sec

Title: US-10-668-767-128
Perfect score: 26800
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....WDFFPVGDCFRKQYEDLMGE 5128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

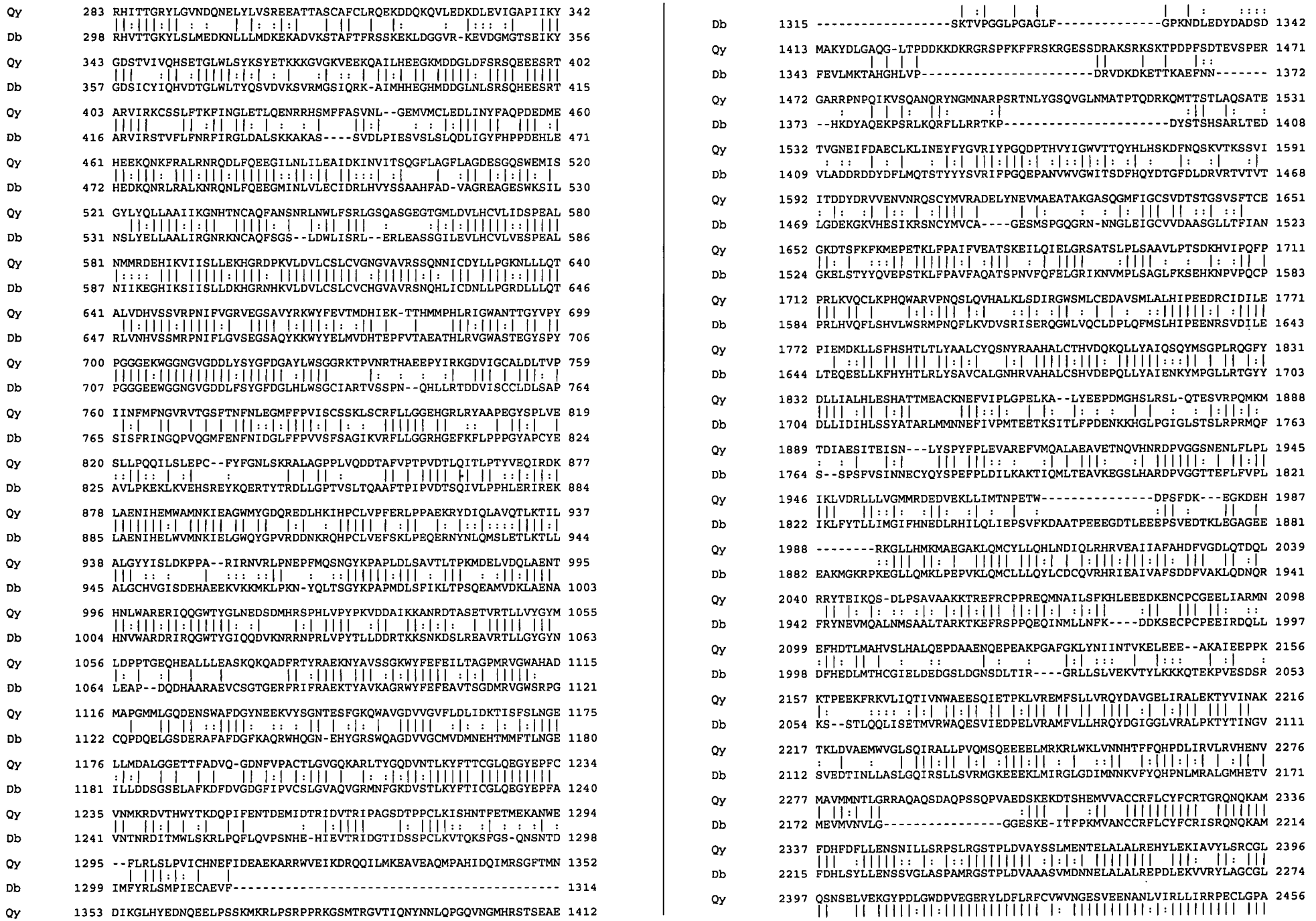
Result No.	Score	% Query Match	Length	DB	ID	Description
1	11887.5	44.4	4968	2	US-09-424-783-5	Sequence 5, Appli
2	11386.5	42.5	4872	2	US-09-424-783-3	Sequence 3, Appli
3	11349	42.3	5037	2	US-09-424-783-4	Sequence 4, Appli
4	11325.5	42.3	5032	2	US-09-538-092-979	Sequence 979, App
5	11295.5	42.1	4866	2	US-09-424-783-2	Sequence 2, Appli
6	658	2.5	2749	2	US-09-385-222A-4	Sequence 4, Appli
7	654	2.4	2713	5	PCT-US96-01735-1	Sequence 1, Appli
8	336.5	1.3	240	1	US-08-114-555A-8	Sequence 8, Appli
9	336.5	1.3	240	2	US-08-559-397A-14	Sequence 14, Appl
10	334.5	1.2	240	1	US-08-114-555A-6	Sequence 6, Appli
11	334.5	1.2	240	2	US-08-559-397A-12	Sequence 12, Appl
12	313.5	1.2	2262	2	US-09-949-016-8849	Sequence 8849, Ap
13	308	1.1	3259	2	US-09-949-016-6507	Sequence 6507, Ap
14	305.5	1.1	5024	2	US-09-710-279-2964	Sequence 2964, Ap
15	305	1.1	2733	2	US-09-949-016-11433	Sequence 11433, A
16	303.5	1.1	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
17	302	1.1	3878	2	US-09-914-259-11	Sequence 11, Appl
18	288	1.1	3248	1	US-08-353-700-1	Sequence 1, Appli
19	288	1.1	3248	5	PCT-US95-16216-1	Sequence 1, Appli
20	285	1.1	3210	2	US-09-538-092-1154	Sequence 1154, Ap
21	276.5	1.0	2954	2	US-09-150-867-1	Sequence 1, Appli
22	276.5	1.0	2954	3	US-09-724-584-1	Sequence 1, Appli
23	263	1.0	200	2	US-10-104-047-3679	Sequence 3679, Ap
24	259.5	1.0	2349	2	US-09-538-092-914	Sequence 914, App
25	255.5	1.0	3433	2	US-09-538-092-1136	Sequence 1136, Ap
26	249.5	0.9	2482	1	US-08-328-254-6	Sequence 6, Appli
27	244.5	0.9	2186	2	US-09-949-016-10828	Sequence 10828, A
28	240.5	0.9	3433	2	US-09-091-501B-10	Sequence 10, Appl
29	222	0.8	604	2	US-09-385-222A-2	Sequence 2, Appli
30	218	0.8	2663	2	US-09-538-092-1252	Sequence 1252, Ap
31	216.5	0.8	2662	2	US-09-595-684B-31	Sequence 31, Appl
32	205.5	0.8	3696	2	US-09-134-001C-5080	Sequence 5080, Ap
33	203.5	0.8	1786	2	US-08-973-462-8	Sequence 8, Appli
34	191	0.7	2141	2	US-09-949-016-10918	Sequence 10918, A
35	190	0.7	1979	2	US-09-949-016-6468	Sequence 6468, Ap
36	190	0.7	2047	2	US-09-949-016-7404	Sequence 7404, Ap
37	190	0.7	2107	2	US-09-949-016-7646	Sequence 7646, Ap
38	190	0.7	2107	2	US-09-949-016-7647	Sequence 7647, Ap
39	187.5	0.7	1939	2	US-09-949-016-11104	Sequence 11104, A
40	187	0.7	2115	2	US-09-296-662-33	Sequence 33, Appl
41	187	0.7	4563	2	US-09-538-092-842	Sequence 842, App
42	185.5	0.7	1530	2	US-09-976-594-736	Sequence 736, App
43	185.5	0.7	1530	2	US-09-949-016-6668	Sequence 6668, Ap
44	185.5	0.7	1938	2	US-09-949-016-6417	Sequence 6417, Ap
45	185	0.7	2154	1	US-08-841-349-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-424-783-5
; Sequence 5, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4968
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-424-783-5

Query Match 44.4%; Score 11887.5; DB 2; Length 4968;
Best Local Similarity 46.7%; Pred. No. 0;
Matches 2459; Conservative 903; Mismatches 1455; Indels 451; Gaps 92;

```
Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              |:||  | |:: ||||:| | | ||||     :::|||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG--------------TGSGHRTLLYGNAI 104
              ||| | ||:||:|||||||:: |   | :|               | ||||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              ||||  | ||| ||||| || ||||||||||: : |||||||:|||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::|||||  :  |    |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   ||||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGGSHIRWGQPFRL 297
```



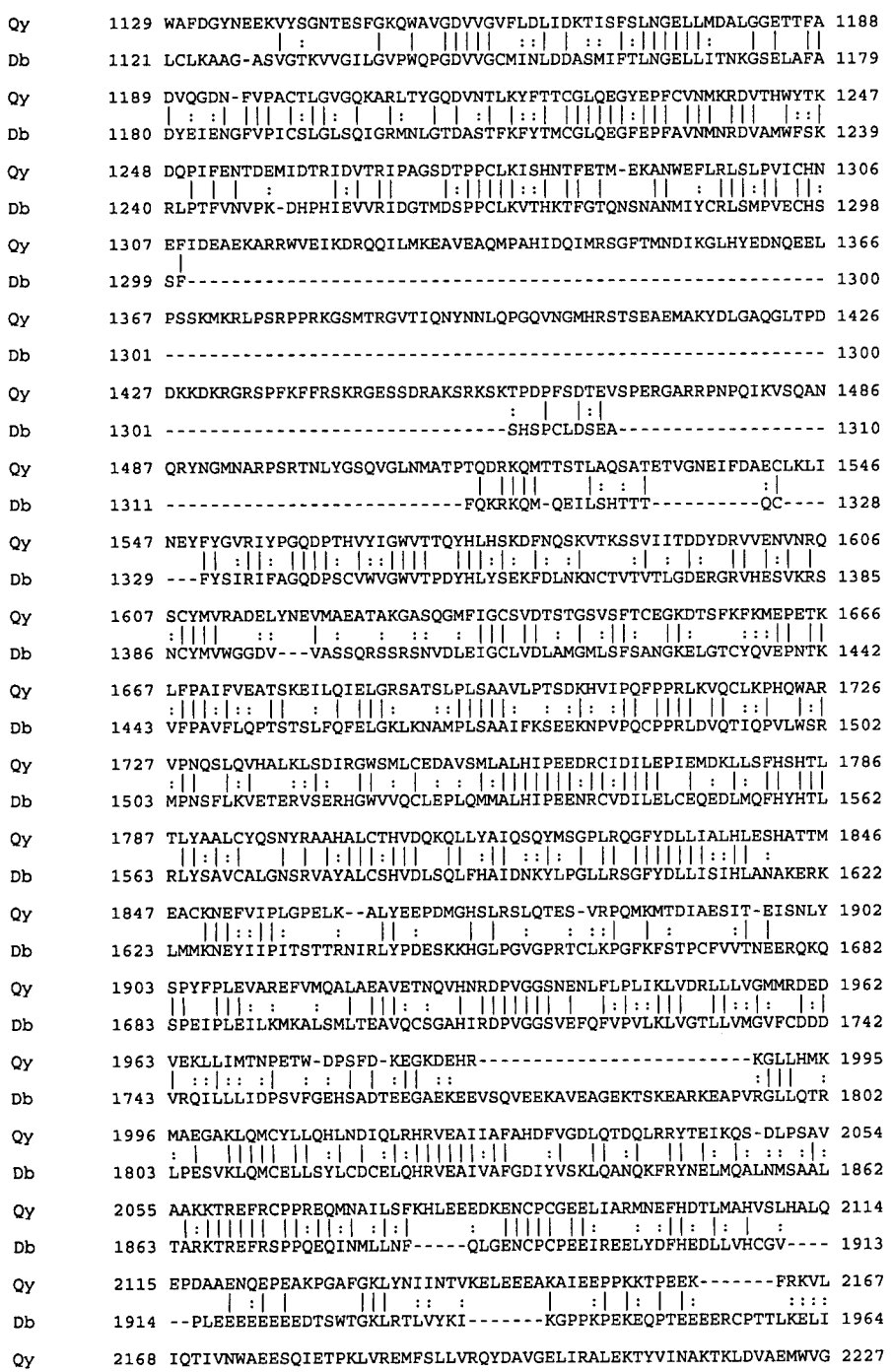

Db 2275 QSCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPA 2334
Qy 2457 LRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPES---------DEDE 2506
Db 2335 LRGEGGNGLLAAMEEAIKIAE----------DPSRDGPSPTSGSSKTLDTEEEED 2379
Qy 2507 DYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLR 2566
Db 2380 DTIHMGNAIMTFYAALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIA 2439
Qy 2567 FTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAA 2626
Db 2440 FQMPTIAKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAA 2499
Qy 2627 TMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNR 2686
Db 2500 ASLDTAALSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGC 2559
Qy 2687 MLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAK 2746
Db 2560 SLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWK 2619
Qy 2747 YYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPP 2806
Db 2620 YYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPP 2678
Qy 2807 DYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWAS 2866
Db 2679 DY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNIIIPEKLEYFINKYAEHSHDKWSM 2734
Qy 2867 RKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEV 2926
Db 2735 DKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR- 2793
Qy 2927 DIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNA 2986
Db 2794 ---EGDSMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENY 2848
Qy 2987 HDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSK 3046
Db 2849 HNIWAKKKKLELESKGGGNHPLLVPYDTLTAKEKAKDREKAQDILKFLQINGYAVSRGFK 2908
Qy 3047 APQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDI 3106
Db 2909 DLELDTP------SIEKRFAYSFLQQLIRYVDEA--HQYILEFDGGSRSKGEHFPYEQEI 2960
Qy 3107 KFFSKAVLPLMEKYFSTHRNYFIAVAT-ATNNVGAASLKEKEMVAALFCKLASLLRSRLA 3165
Db 2961 KFFAKVVLPLIDQYFKNHRLYFLSAASRPLCSGGHASNKEKEMVTSLFCKLGVLVRHRIS 3020
Qy 3166 AFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKY 3225
Db 3021 LFGNDATSIVNCLHILGQTLDARTVMKTGLESVKSALRAFLDNAAEDLEKTMENLKQGQF 3080
Qy 3226 AHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYAL 3285
Db 3081 THTRNQPRGVTQIINYTTVALLPMLSSLFEHIGQHQFGEDLILEDVQVSCYRILTSLYAL 3140
Qy 3286 GTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHS 3345
Db 3141 GTSKSI---------YVERQRSALGECLAAFAGAFPVAFLETHLNKHNIYSIYNTKSSRE 3191
Qy 3346 LEAQDIMQKMEQ-C--MPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWA 3402
Db 3192 RAALSLPANVEDVCPNIPSLEKLMEEIVELAESGIRYTQMPHVMEVILPMLCSYMSRWWE 3251
Qy 3403 QGPDNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSS 3462
Db 3252 HGPESNPGRAEMCCTALNSEHMNTLLGNILKIIYNNLGIDEGAWMKRLAVFSQPIINKVK 3311
Qy 3463 EELLRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYS 3522
Db 3312 PQLLKTHFLPLMEKLKKKAAMVVSEEDHLKA---EARGDMSEAELLILDEFTTLARDLYA 3368
Qy 3523 FYPLLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNM 3582
Db 3369 FYPLLIRFVDYNRAKWLKEPTPEAEELFRMVAEVFIYWSKSHNFKREEQNFVVQNEINNM 3428
Qy 3583 VLIMPTATRRVT--AVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLN 3640
Db 3429 SFLITDTKSKMSKAAVSD--------QERKKMKRKGDR-YSMQTSLIVAALKRLLPIGLN 3479
Qy 3641 LFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKI-DPADEMSWQHYLYSKLGSK 3699
Db 3480 ICAPGDQELIALAKNRFSLKDTEDEVRDIIRNNIHLQGKLEDPA--IRWQMALY-----K 3532
Qy 3700 SKSNITVETAENKAKIIDDTVERIVAMSKVLFGL-----------HMIDHPQQMSKNVY 3747
Db 3533 DLPNRTEETSDP-----EKTVERVLDIANVLFHLEQKSKFIGRRYYNLVEHPQRSKKAVW 3587
Qy 3748 RSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLE-EENIGQEVMIEDLTQS 3806
Db 3588 HKLLSKQRKRAVVACFRMAPLYNLPRHRAVNLFLQGYEKSWIETEEHYFEDKLIEDLAK- 3646
Qy 3807 FEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEE 3866
Db 3647 -PGAEPPEED--EVTKRVDPLHQLILLFSRTALTEKC-KLEEDFLYMAYADIMAKSCHDE 3702
Qy 3867 EEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKG 3926
Db 3703 EDDDGEEEVK-----------SFEEKEMEKQKLLYQQARLHDRGAAEMVLQTISASKG 3749
Qy 3927 LPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFE 3986
Db 3750 ETGPMVAATLKLGIAILNGGNSTVQQKMLDYLKEKKDVGFFQSLAGLMQSCSVLDLNAFE 3809
Qy 3987 RNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVN 4046
Db 3810 RQNKAEGLGMVTEEGSGEKVLQDDEFTCDLFRFLQLLCEGHNSDFQNYLRTQTGNNTTVN 3869
Qy 4047 VVICTVDYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCT 4106
Db 3870 IIISTVDYLLRVQESISDFYWYYSGKDVIDEQGQRNFSKAIQVAKQVFNTLTEYIQGPCT 3929
Qy 4107 QNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGN 4166
Db 3930 GNQQSLAHSRLWDAVVGFLHVFAHMQMKLSQDSSQIELLKELMDLQKDMVVMLLSMLEGN 3989
Qy 4167 VVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFK 4226
Db 3990 VVNGTIGKQMVDMLVESSNNVEMILKFFDMFLKLKDLTSSDTFKEYDPDGKGIISKRDFH 4049
Qy 4227 EKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHM 4286
Db 4050 KAMESHKHYTQSETEFLLSCAETDENETLDYEEFVKRFHEPAKDIGFNVAVLLTNLSEHM 4109
Qy 4287 PNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESK 4346
Db 4110 PNETRLQTFLELAESVLNYFQPFLGRIEIMGSAKRIERVYFEISESSRTQWEKPQVKESK 4169
Qy 4347 RAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVG-GTKNREASYMYMG 4405
Db 4170 RQFIFDVVNEGGEKEKMELFVNFCEDTIFEMQLAAQI---SESDLNERSANKEESEK--- 4223
Qy 4406 DDDDERAGKDPF------RRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGF 4459
Db 4224 ERPEEQGPKMGFFSVLTVRSALFALRYNILTLMRMLSLKSLKKQMKKMKKMTVKDMVTAF 4283
Qy 4460 FKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPP-----------PEPTEEEKI 4507
Db 4284 FSSYWSIFMTLLHFVASVFRGFFRIVCSLLLGGSLVEGAKKIKVAELLANMPDPTQDEVR 4343
Qy 4508 GQ----LRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESPSTS 4563
Db 4344 GDGEEGERKPMETTLPSEDLTDLKELTEESDLLSDIFGLDL-KREGGQYKLIPH------ 4396

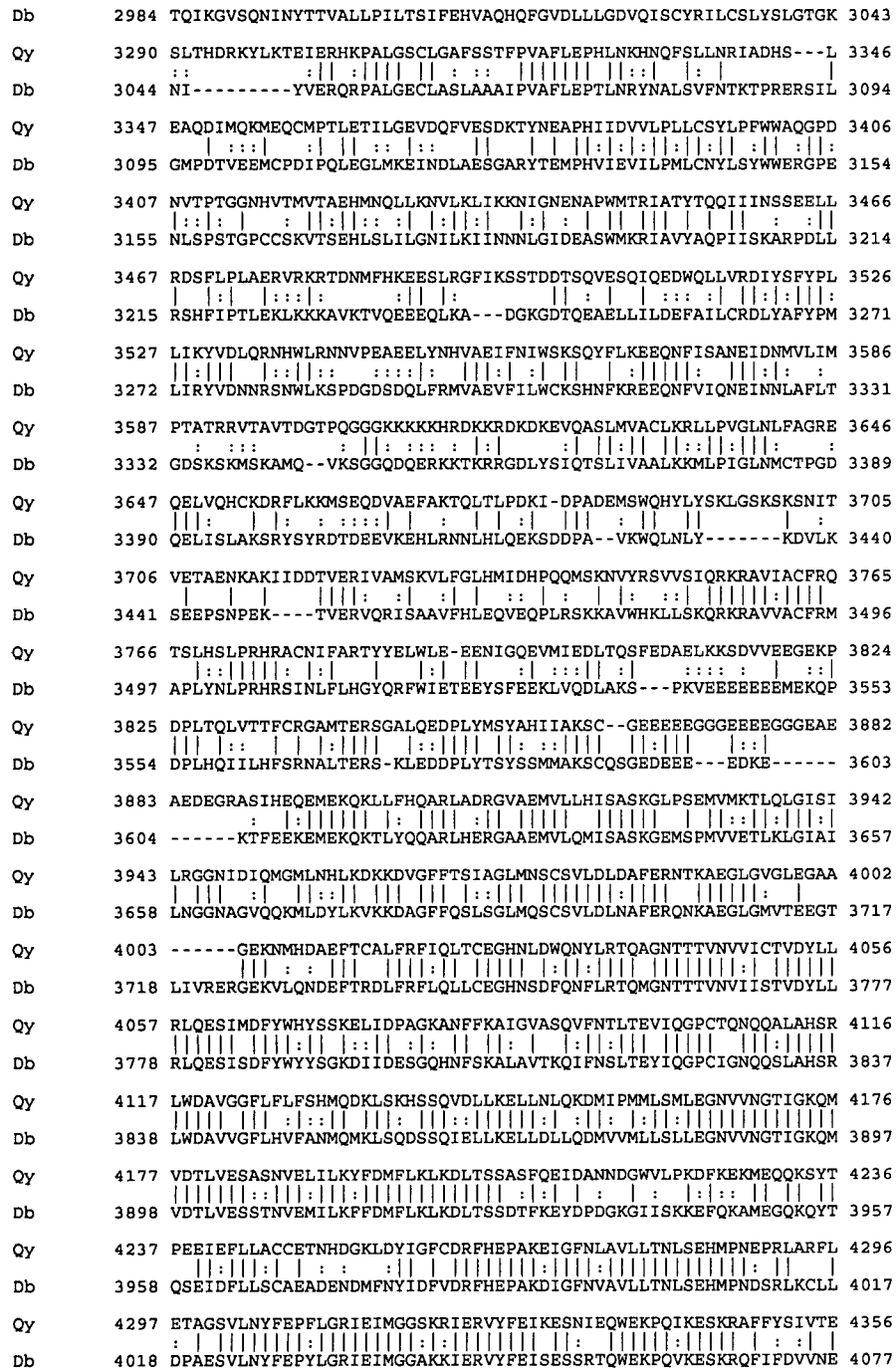
```
Qy       4564 TPSSG-----------------EEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQE 4605
Db       4397 NPNAGLSDLMSNPVLIPEEQEKFQEQKTKEEEKEEKEETKSEPEKAEGEDGEKEEKVKED 4456

Qy       4606 RMEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALV 4665
Db       4457 KGKQKLRQLHTHRYGEPE--------VPESAFWKKIIAYQQKLLNYFARNFYNMRMLALF 4508

Qy       4666 LAFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEV 4725
Db       4509 VAFAINFILLFYKVST-----------SSVVEGKELPSRSTSENAKVTTSLDSSSHRIIA 4557

Qy       4726 VH--IDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLY 4783
Db       4558 VHYVLEESSGYMEPTLRILAILHTVISFFCIIGYYCLKVPLVIFKREKEVARKLEFDGLY 4617

Qy       4784 IAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTS 4843
Db       4618 ITEQPSEDDIKGQWDRLVINTQSFPNNYWDKFVKRKVMDKYGEFYGRDRISELLGMDKAA 4677

Qy       4844 F---SAQEEEGSK---GLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNN 4897
Db       4678 LDFSDAREKKKPKKDSSLSAVLNSIDVKYQMWKLGVVFTDNSFLYLAWYMTMSILGHYNN 4737

Qy       4898 FFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQE 4957
Db       4738 FFFAAHLLDIAMGFKTLRTILSSVTHNGKQLVLTVGLLAVVVYLYTVVAFNFFRKFYNKS 4797

Qy       4958 ED-DEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIV 5016
Db       4798 EDGDTPDMKCDDMLTCYMFHMYVGVRAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVIV 4857

Qy       5017 ILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLA 5076
Db       4858 ILLAIIQGLIIDAFGELRDQQEQVKEDMETKCFICGIGNDYFDTVPHGFETHTLQEHNLA 4917

Qy       5077 NYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYED 5124
Db       4918 NYLFFLMYLINKDETEHTGQESYVWKMYQERCWEFFPAGDCFRKQYED 4965
```

RESULT 2
US-09-424-783-3
; Sequence 3, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4872
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-424-783-3

Query Match 42.5%; Score 11386.5; DB 2; Length 4872;
Best Local Similarity 44.8%; Pred. No. 0;
Matches 2359; Conservative 911; Mismatches 1462; Indels 531; Gaps 90;

```
Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIATVHKEQRKFCLAAEGLGNRLCFLEPTSEAKFIPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAILLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        122 CLTTSRSQTDKLAFDVGLREHATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
Db        182 LHLSISNGNIQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        240 DQNDSQHRRIFYEAGGAGTRARSLWRVEPLRISWSGSNIRWGQAFRLRHLTTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQV--LEDKDLEVIGAPIIKYGDSTVIVQHSE 353
Db        300 DQGLLLQDRGKADTKSTAFSFRPSKETKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHIA 359

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
Db        360 SGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTALF 418

Qy        414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
Db        419 SQFVSG-----NNRTAAP--VTLPIEEVLQTLHDLIAYFQPPEEEMQHEDKQNKLRSLKN 471

Qy        474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
Db        472 RQNLFKEEGMLALVLNCIDRLNIYNSVAHFAG-IAREESGMAWKEVLSLLYKLLAALIRG 530

Qy        534 NHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIIS 593
Db        531 NRNTCAQF--SNNLDWLISKLDRLES--SSGILEVLHCILIESPEALNLIAEGHIKSIIS 586

Qy        594 LLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNI 653
Db        587 LLDKHGRNHKVLDVLCSLCLCNGVAVRANQNLICDNLLPRRNLLLQTRLINDVTSIRPNI 646

Qy        654 FVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVG 712
Db        647 FLGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASSSGYAPYPGGGEGWGGNGVG 706

Qy        713 DDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTG 772
Db        707 DDLYSYGFDGLHLWSG--RIPRAVASINQHLLKSDDVVSCCLDLGVPSISFRINGQPVQG 764

Qy        773 SFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPC 832
Db        765 MFENFNTDGLFFPVMSFSAGVKVRFLMGGRHGEFKFLPPSGYAPCYEALLPKEKMRLEPV 824

Qy        833 FYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNK 890
Db        825 KEYKRDAEGVRDLLGTTQFLSQASFIPCPIDTSQVVLPPHLEKIRDRLAENIHELWGMNK 884

Qy        891 IEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPA 950
Db        885 IELGWTFGKMRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLALGCHIAHVNPAA 944

Qy        951 R--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGW 1008
Db        945 EEDLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWAKDRIKQGW 1003

Qy       1009 TYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALL 1068
Db       1004 TYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFVGYGYNIEPSDQELADPAV 1063

Qy       1069 LEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENS 1128
Db       1064 EKVSIDK---IRFFRVERSYAVRSGKWYFEFEVVTGGDMRVGWARPGCRPDIELGPMTKP 1120
```

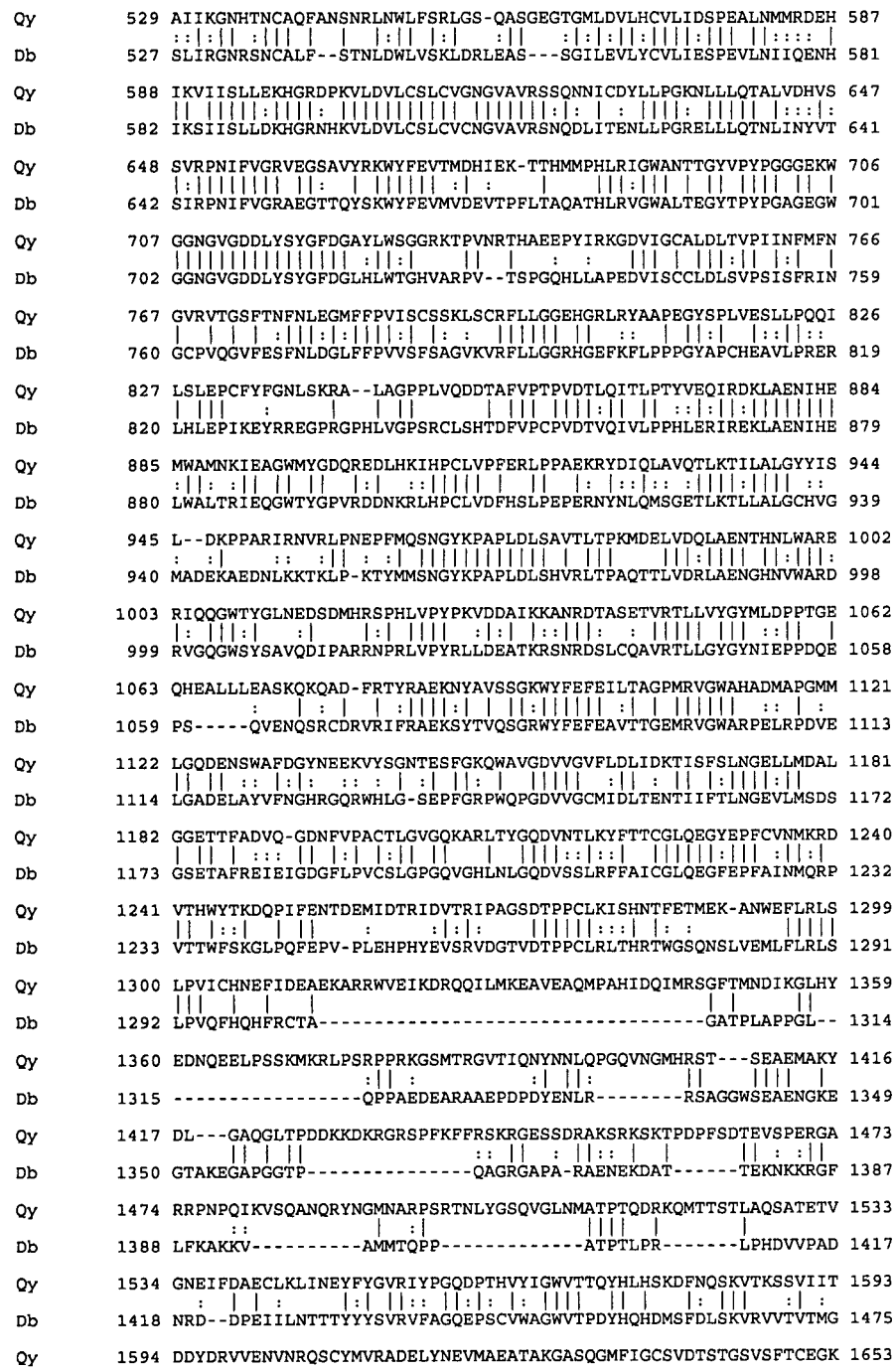

Qy 1129 WAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFA 1188
Db 1121 LCLKAAG-ASVGTKVVGILGVPWQPGDVVGCMINLDDASMIFTLNGELLITNKGSELAFA 1179
Qy 1189 DVQGDN-FVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTK 1247
Db 1180 DYEIENGFVPICSLGLSQIGRMNLGTDASTFKFYTMCGLQEGFEPFAVNMNRDVAMWFSK 1239
Qy 1248 DQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETM-EKANWEFLRLSLPVICHN 1306
Db 1240 RLPTFVNVPK-DHPHIEVVRIDGTMDSPPCLKVTHKTFGTQNSNANMIYCRLSMPVECHS 1298
Qy 1307 EFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEEL 1366
Db 1299 SF---------- 1300
Qy 1367 PSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPD 1426
Db 1301 ---------- 1300
Qy 1427 DKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQAN 1486
Db 1301 ----------SHSPCLDSEA---------- 1310
Qy 1487 QRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLI 1546
Db 1311 ----------FQKRKQM-QEILSHTTT----------QC---- 1328
Qy 1547 NEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQ 1606
Db 1329 ---FYSIRIFAGQDPSCVWVGWVTPDYHLYSEKFDLNKNCTVTVTLGDERGRVHESVKRS 1385
Qy 1607 SCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETK 1666
Db 1386 NCYMVWGGDV---VASSQRSSRSNVDLEIGCLVDLAMGMLSFSANGKELGTCYQVEPNTK 1442
Qy 1667 LFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWAR 1726
Db 1443 VFPAVFLQPTSTSLFQFELGKLKNAMPLSAAIFKSEEKNPVPQCPPRLDVQTIQPVLWSR 1502
Qy 1727 VPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTL 1786
Db 1503 MPNSFLKVETERVSERHGWVVQCLEPLQMMALHIPEENRCVDILELCEQEDLMQFHYHTL 1562
Qy 1787 TLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTM 1846
Db 1563 RLYSAVCALGNSRVAYALCSHVDLSQLFHAIDNKYLPGLLRSGFYDLLISIHLANAKERK 1622
Qy 1847 EACKNEFVIPLGPELK--ALYEEPDMGHSLRSLQTES-VRPQMKMTDIAESIT-EISNLY 1902
Db 1623 LMMKNEYIIPITSTTRNIRLYPDESKKHGLPGVGPRTCLKPGFKFSTPCFVVTNEERQKQ 1682
Qy 1903 SPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDED 1962
Db 1683 SPEIPLEILKMKALSMLTEAVQCSGAHIRDPVGGSVEFQFVPVLKLVGTLLVMGVFCDDD 1742
Qy 1963 VEKLLIMTNPETW-DPSFD-KEGKDEHR----------KGLLHMK 1995
Db 1743 VRQILLLIDPSVFGEHSADTEEGAEKEEVSQVEEKAVEAGEKTSKEARKEAPVRGLLQTR 1802
Qy 1996 MAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAV 2054
Db 1803 LPESVKLQMCELLSYLCDCELQHRVEAIVAFGDIYVSKLQANQKFRYNELMQALNMSAAL 1862
Qy 2055 AAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQ 2114
Db 1863 TARKTREFRSPPQEQINMLLNF-----QLGENCPCPEEIREELYDFHEDLLVHCGV---- 1913
Qy 2115 EPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEK-------FRKVL 2167
Db 1914 --PLEEEEEEEEDTSWTGKLRTLVYKI-------KGPPKPEKEQPTEEEERCPTTLKELI 1964
Qy 2168 IQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVG 2227
Db 1965 SQTMIRWAQEDQIQDAELVRMMFNLLRRQYDSIGELLQALRKTYTISHASVSDTINLLAA 2024
Qy 2228 LSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRR 2287
Db 2025 LGQIRSLLSVRMGREEELLMINGLGDIMNNKVFYQHPNLMRVLGMHETVMEVMVNVLG-- 2082
Qy 2288 AQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENS 2347
Db 2083 ----------TEKSQIAFPKMVASCCRFLCYFCRISRQNQKAMFEHLSYLLENS 2126
Qy 2348 NILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGY 2407
Db 2127 SVGLASPSMRGSTPLDVAASSVMDNNELALGLEEPDLEKVVTYLAGCGLQSCPMLLAKGY 2186
Qy 2408 PDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLK 2466
Db 2187 PDVGWNPIEGERYLSFLRFAVFVNSESVEENASVVVKLLIRRPECFGPALRGEGGNGLLA 2246
Qy 2467 AIVDANKMSERIADRRKLREMEQEGDVNFSHPLPE-SDEDEDYIDTGAAILNFYCTLVDL 2525
Db 2247 AMQGAIKISESPA-----LDLPSQG---YKREVPEDGEEEEEIVHMGNAIMSFYSALIDL 2298
Qy 2526 LGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKS--DM 2583
Db 2299 LGRCAPEMHLIQTGKGEAIRIRSILRSLVPTEDLVGIISIPLKL--PSLNKDGSVSEPDM 2356
Qy 2584 PSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSM 2643
Db 2357 AANFCPDHKAPMVLFLDRVYGIKDQTFLLHLLEVGFLPDLRASASLDTVALSTTESALAL 2416
Qy 2644 NRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVAL 2703
Db 2417 NRYICSAVLPLLTRCAPLFAGTEHYTSLIDSTLQTIYRLSKGRSLTKAQRDTIEECLLAI 2476
Qy 2704 TSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSD 2763
Db 2477 CNHLRPSMLQQLLRRLVFDVPQLNDYCKMPLKLLTNHFEQCWKYY-CLPSGWGSYGLAVE 2535
Qy 2764 EEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDY-------SLSKNYDD 2816
Db 2536 EELHLTEKLFWGIFDSLSHKKYDPDLFRMSLPCLSAIAGALPPDYLDTRITATLEK---- 2591
Qy 2817 EFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYG 2876
Db 2592 ------QVSVDADG-NFDPKPINTINFSLPEKLEYIVTKYAEHSHDKWACEKSQSGWKYG 2644
Qy 2877 EGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE-----VDIPSN 2931
Db 2645 ISLDENVKTHPLIRPFKTLTEKEKEIYRWPARESLKTMLAVGWTVERTKEGEALVQLREN 2704
Qy 2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
Db 2705 EKLRSVSQTSQGN----------SYNPAPLDLSNVVLSRELQGMVEVVAENYHNIWA 2751
Qy 2992 KKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSD 3051
Db 2752 KKKKLELESKGGGSHPLLVPYDTLTAKEKFRDREKAQDLFKFLQVNGVIVSRGMKDMELD 2811
Qy 3052 TEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSK 3111
Db 2812 ------AFSMEKRFAYKFLKKILKYVDSAQEFIAHLE-AIVSSGKTEKSPHDQEIKFFAK 2864
Qy 3112 AVLPLMEKYFSTHRNYFI-AVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPD 3170
Db 2865 VLLPLVDQYFTNHRLYFLSSPLKPLSSSGYASHKEKEMVASLFCKLAALVRHRISLFGSD 2924
Qy 3171 VRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRG 3230
Db 2925 STTMVSCLHILAQTLDTRTVMKSGSELVKAGLRAFFESAAEDLEKTSENLKLGKFTHSR- 2983
Qy 3231 THLK-TSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDA 3289

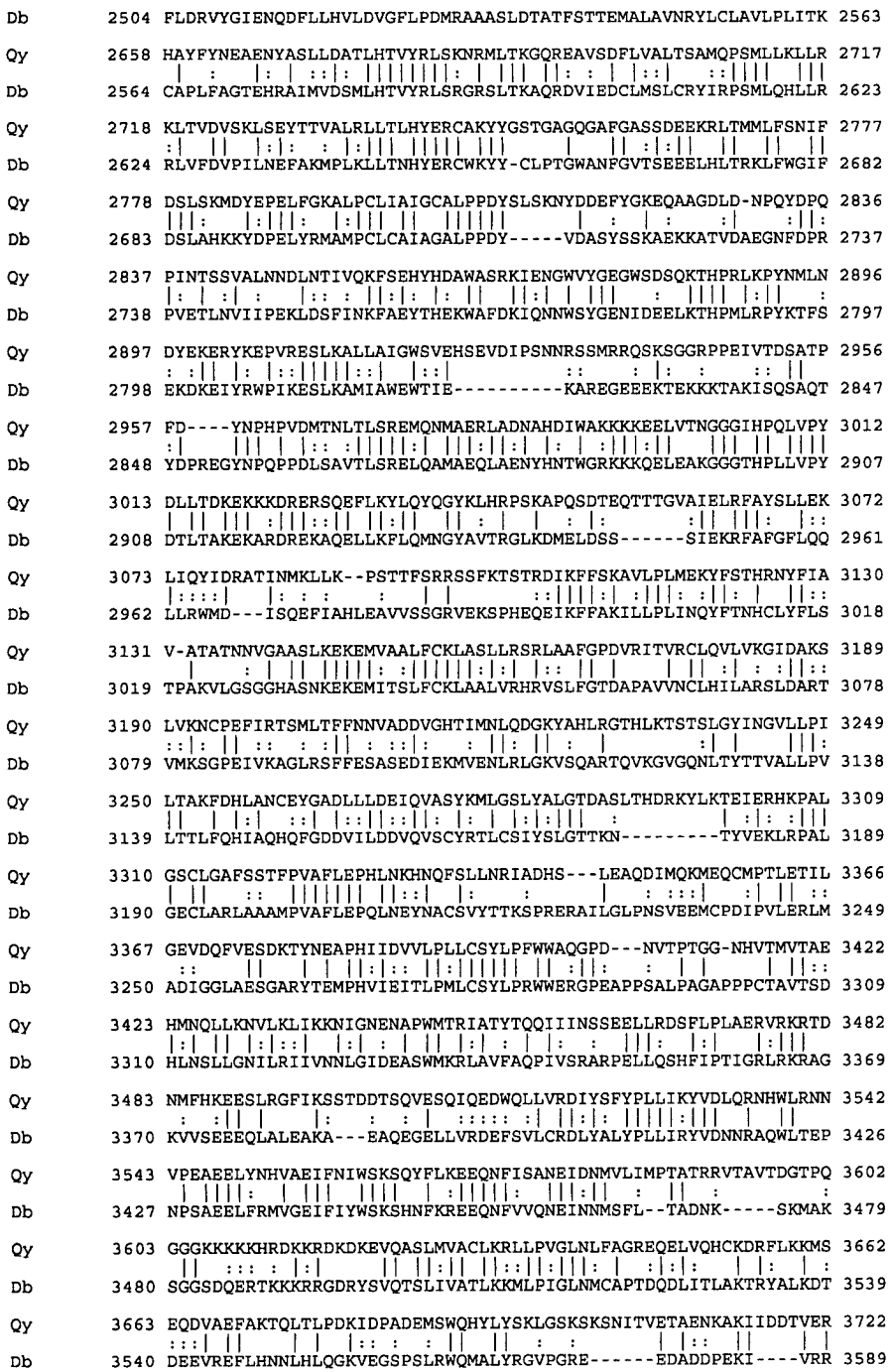


RESULT 3
US-09-424-783-4
; Sequence 4, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18

```
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;    LENGTH: 5037
;    TYPE: PRT
;    ORGANISM: Oryctolagus cuniculus
US-09-424-783-4

  Query Match             42.3%;  Score 11349;  DB 2;  Length 5037;
  Best Local Similarity   44.9%;  Pred. No. 0;
  Matches 2395;  Conservative  906;  Mismatches 1517;  Indels  516;  Gaps  106;

Qy          5 EGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPPD 59
Db          3 DGGEGE-DEVQFLRTDDEVVLQCSATVLKEQLKLCLAAEGFGNRLCFLEPTSNAQNVPPD 61

Qy         60 LSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 LAICCFTLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSRMYLS 119

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        120 CLTTSRSMTDKLAFDVGLQEDATGEACWWTMHPASKQRSEGEKVRVGDDLILVSVSSERY 179

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIPS 234
Db        180 LHLSTASGELQVDASFMQTLWNMNP----ICSCCEEGYVTGGHVLRLFHGHMDECLTI-S 234

Qy        235 TWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVN 294
Db        235 AADSDDQRRLVYYEGGAVCTHARSLWRLEPLRISWSGSHLRWGQPLRIRHVTTGRYLALT 294

Qy        295 DQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
Db        295 EDQGLVVVDACKAHTKATSFCFRVSK-EKLDTAPKRDVEGMGPPEIKYGESLCFVQHVAS 353

Qy        355 GLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFT 414
Db        354 GLWLTYAAPDPKALRLG-VLKKKAILHQEGHMDDALFLTRCQQEESQAARMIHSTAGLYN 412

Qy        415 KFINGLETLQENRRHSMFFA--SVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
Db        413 QFIKGLDSFSGKPRGSGPPAGPALPIEAVILSLQDLIGYFEPPSEELQHEEKQSKLRSLR 472

Qy        473 NRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIK 532
Db        473 NRQSLFQEEGMLSLVLNCIDRLNVYTTAAHFAEY-AGEEAAESWKEIVNLLYELLASLIR 531

Qy        533 GNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVI 591
Db        532 GNRANCALF--STNLDWVVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENHIKSI 586

Qy        592 ISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRP 651
Db        587 ISLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQDLITENLLPGRELLLQTNLINYVTSIRP 646

Qy        652 NIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKWGGNG 710
Db        647 NIFVGRAEGSTQYGKWYFEVMVDEVVPFLTAQATHLRVGWALTEGYSPYPGGGEGWGGNG 706

Qy        711 VGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRV 770
Db        707 VGDDLYSYGFDGLHLWTGHVARPV--TSPGQHLLAPEDVVSCCLDLSVPSISFRINGCPV 764

Qy        771 TGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLE 830
Db        765 QGVFEAFNLDGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRERLRLE 824

Qy        831 PCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAM 888
Db        825 PIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHELWAL 884

Qy        889 NKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL--D 946
Db        885 TRIEQGWTYGPVRDDNKRLHPCLVNFHSLPEPERNYNLQMSGETLKTLLALGCHVGMADE 944

Qy        947 KPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQ 1006
Db        945 KAEDNLKKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARDRVAQ 1003

Qy       1007 GWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEA 1066
Db       1004 GWSYSAVQDIPARRNPRLVPYRLLDEATKRSNRDSLCQAVRTLLGYGYNIEPPDQEPS-- 1061

Qy       1067 LLLEASKQKQAD-FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQD 1125
Db       1062 ---QVENQSRWDRVRIFRAEKSYTVQSGRWYFEFEAVTTGEMRVGWARPELRPDVELGAD 1118

Qy       1126 ENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGET 1185
Db       1119 ELAYVFNGHRGQRWHLG-SEPFGRPWQSGDVVGCMIDLTENTIIFTLNGEVLMSDSGSET 1177

Qy       1186 TFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHW 1244
Db       1178 AFREIEIGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFAICGLQEGFEPFAINMQRPVTTW 1237

Qy       1245 YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEK-ANWEFLRLSLPVI 1303
Db       1238 FSKSLPQFEPVPPE-HPHYEVARMDGTVDTPPCLRLAHRTWGSQNSLVEMLFLRLSLPVQ 1296

Qy       1304 CHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQ 1363
Db       1297 FHQHFRCTA---------------------------------GAT------------- 1308

Qy       1364 EELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGL 1423
Db       1309 -----------PLAPP---------------GLQP---------PAEDE-------ARAA 1326

Qy       1424 TPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVS 1483
Db       1327 EPDPDYENLRRSAGGWGEAEGGKEGTAKEGTPGGTPQP--GVEAQP---VRAENEKDATT 1381

Qy       1484 QANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETV-GNEIFDAEC 1542
Db       1382 EKNKK---------RGFLFKAKKAAMMTQPP------ATPALPRLPHDVVPADNRDDPEI 1426

Qy       1543 LKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVEN 1602
Db       1427 ILNTTTYYYSVRVFAGQEPSCVWVGWVTPDYHQHDMNFDLSKVRAVTVTMGDEQGNVHSS 1486

Qy       1603 VNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKME 1662
Db       1487 LKCSNCYMVWGGDF---VSPGQQGRISHTDLVIGCLVDLATGLMTFTANGKESNTFFQVE 1543

Qy       1663 PETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPH 1722
Db       1544 PNTKLFPAVFVLPTHQNVIQFELGKQKNIMPLSAAMFLSERKNPAPQCPPRLEVQMLMPV 1603

Qy       1723 QWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFH 1782
Db       1604 SWSRMPNHFLQVETRRAGERLGWAVQCQDPLTMMALHIPEENRCMDILELSERLDLQRFH 1663

Qy       1783 SHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESH 1842
Db       1664 SHTLRLYRAVCALGNNRVAHALCSHVDQAQLLHALEDAHLPGPLRAGYYDLLISIHLESA 1723

Qy       1843 ATTMEACKNEFVIPLGPELKALYEEPD-------MGHSLRSL-QTESVRPQMKMTD---- 1890
Db       1724 CRSRRSMLSEYIVPLTPETRAITLFPPGRKGGNARRHGLPGVGVTTSLRPPHHFSPPCFV 1783

Qy       1891 ---IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIK 1947
Db       1784 AALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHARDPVGGSVEFQFVPVLK 1843
```

```
Db       3899 FQNYLRTQTGNTTTINIIICTVDYLLRLQESISDFYWYYSGKDVIEEQGKRNFSKAMSVA 3958

Qy       4091 SQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLN 4150

Db       3959 KQVFNSLTEYIQGPCTGNQQSLAHSRLWDAVVGFLHVFAHMMMKLAQDSSQIELLKELLD 4018

Qy       4151 LQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQ 4210

Db       4019 LQKDMVVMLLSLLEGNVVNGMIARQMVDMLVESSSNVEMILKFFDMFLKLKDIVGSEAFQ 4078

Qy       4211 EIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKE 4270

Db       4079 DYVTDPRGLISKKDFQKAMDSQKQFTGPEIQFLLSCSEADENEMINFEEFANRFQEPARD 4138

Qy       4271 IGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIK 4330

Db       4139 IGFNVAVLLTNLSEHVPHDPRLRNFLELAESILEYFRPYLGRIEIMGASRRIERIYFEIS 4198

Qy       4331 ESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEES 4390

Db       4199 ETNRAQWEMPQVKESKRQFIFDVVNEGGEAEKMELFVSFCEDTIFEMQIAAQISEPEGEP 4258

Qy       4391 VGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDG----------------------V 4428

Db       4259 -------EA-------DEDEGMGE----AAAEGAEEGAAGAEGAAGTVAAGATARLAAAA 4300

Qy       4429 ATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGY----GVLVVVRYIFGV 4484

Db       4301 ARALRGLSYRSLRRRVRRLRRLTAREAATALAALLWAVVARAGAAGAGAAAGALRLLWGS 4360

Qy       4485 LL--GLMRGPQ----TD--EPPPEPTEEEKIGQLRHRLLATQSSRHLPALP--PADDTGQ 4534

Db       4361 LFGGGLVEGAKKVTVTELLAGMPDPTSDEVHGE------------QPAGPGGDADGAGE 4407

Qy       4535 MQVSAFGLDITKEDNGQIQVKPHES---------------------------------- 4559

Db       4408 GE----GEGDAAEGDGDEEVAGHEAGPGGAEGVVAVADGGPFRPEGAGGLGDMGDTTPAE 4463

Qy       4560 PSTSTPS---------SGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQ 4610

Db       4464 PPTPEGSPILKRKLGVDGEEEELVPE---PEPEPEPEPEKADEENGE--KEEVPE----- 4513

Qy       4611 AAQQAAMSAIEAESKKAVQGPAPSALSQV----------DLSQYTRRAVSFLARNFYNLK 4660

Db       4514 --------APPEPPKKA--PPSPPAKKEEAGGAGMEFWGELEVQRVKFLNYLSRNFYTLR 4563

Qy       4661 YVALVLAFCINFVLLFYKVSTLDGEGG----EGSGLGDIIAGGGSGSGAGSGSGDGSGES 4716

Db       4564 FLALFLAFAINFILLFYKVS--DSPPGEDDMEGSAAGD-LAGAGSGGGSGWGSGAGEEAE 4620

Qy       4717 GEDDDALEVVHIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARK 4776

Db       4621 GDEDENMVYYFLEESTGYMEPALWCLSLLHTLVAFLCIIGYNCLKVPLVIFKREKELARK 4680

Qy       4777 LEFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNM 4836

Db       4681 LEFDGLYITEQPGDDDVKGQWDRLVLNTPSFPSNYWDKFVKRKVLDKHGDIFGRERIAEL 4740

Qy       4837 LGM-----EKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSV 4891

Db       4741 LGMDLASLEITAHNERKPDPPPGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLGWYMVMSL 4800

Qy       4892 MGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFR 4951

Db       4801 LGHYNNFFFAAHLLDIAMGVKTLRTILSSVTHNGKQLVMTVGLLAVVVYLYTVVAFNFFR 4860

Qy       4952 KFYVQEED-DEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISF 5010

Db       4861 KFYNKSEDEDEPDMKCDDMMTCYLFHMYVGVRAGGGIGDEIEDPAGDEYELYRVVFDITF 4920

Qy       5011 FFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQ 5070

Db       4921 FFFVIVILLAIIQGLIIDAFGELRDQQEQVKEDMETKCFICGIGSDYFDTTPHGFETHTL 4980

Qy       5071 REHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYED 5124

Db       4981 EEHNLANYMFFLMYLINKDETEHTGQESYVWKMYQERCWDFFPAGDCFRKQYED 5034


RESULT 4
US-09-538-092-979
; Sequence 979, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 979
;   LENGTH: 5032
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P21817
US-09-538-092-979

  Query Match             42.3%;  Score 11325.5;  DB 2;  Length 5032;
  Best Local Similarity   44.9%;  Pred. No. 0;
  Matches 2394;  Conservative  895;  Mismatches 1531;  Indels  513;  Gaps  102;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KN 55

Db          1 MGDAEG----EDEVQFLRTDDEVVLQCSATVLKEQLKLCLAAEGFGNRLCFLEPTSNAQN 56

Qy         56 IPPDLSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSD 112

Db         57 VPPDLAICCFVLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSR 114

Qy        113 MYLACLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVA 171

Db        115 MYLSCLTTSRSMTDKLAFDVGLQEDATGEACWWTMHPASKQRSEGEKVRVGDDIILVSVS 174

Qy        172 TERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECL 230

Db        175 SERYLHLSTASGELQVDASFMQTLWNMNPI---CSRCE-EGFVTGGHVLRLFHGHMDECL 230

Qy        231 TIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRY 290

Db        231 TI-SPADSDDQRRLVYYEGGAVCTHARSLWRLEPLRISWSGSHLRWGQPLRVRHVTTGQY 289

Qy        291 LGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQ 350

Db        290 LALTEDQGLVVVDASKAHTKATSFCFRISK-EKLDVAPKRDVEGMGPPEIKYGESLCFVQ 348

Qy        351 HSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCS 410

Db        349 HVASGLWLTYAAPDPKALRLG-VLKKKAMLHQEGHMDDALSLTRCQQEESQAARMIHSTN 407

Qy        411 SLFTKFINGLETLQENRRHS--MFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKF 468

Db        408 GLYNQFIKSLDSFSGKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPSEDLQHEEKQSKL 467

Qy        469 RALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLA 528

Db        468 RSLRNRQSLFQEEGMLSMVLNCIDRLNVYTTAAHFAEF-AGEEAAESWKEIVNLLYELLA 526
```


Qy 529 AIIKGNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEH 587
Db 527 SLIRGNRSNCALF--STNLDWLVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENH 581
Qy 588 IKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVS 647
Db 582 IKSIISLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQDLITENLLPGRELLLQTNLINYVT 641
Qy 648 SVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKW 706
Db 642 SIRPNIFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQATHLRVGWALTEGYTPYPGAGEGW 701
Qy 707 GGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFN 766
Db 702 GGNGVGDDLYSYGFDGLHLWTGHVARPV--TSPGQHLLAPEDVISCCLDLSVPSISFRIN 759
Qy 767 GVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQI 826
Db 760 GCPVQGVFESFNLDGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRER 819
Qy 827 LSLEPCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHE 884
Db 820 LHLEPIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHE 879
Qy 885 MWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYIS 944
Db 880 LWALTRIEQGWTYGPVRDDNKRLHPCLVDFHSLPEPERNYNLQMSGETLKTLLALGCHVG 939
Qy 945 L--DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARE 1002
Db 940 MADEKAEDNLKKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARD 998
Qy 1003 RIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGE 1062
Db 999 RVGQGWSYSAVQDIPARRNPRLVPYRLLDEATKRSNRDSLCQAVRTLLGYGYNIEPPDQE 1058
Qy 1063 QHEALLLEASKQKQAD-FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMM 1121
Db 1059 PS-----QVENQSRCDRVRIFRAEKSYTVQSGRWYFEFEAVTTGEMRVGWARPELRPDVE 1113
Qy 1122 LGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDAL 1181
Db 1114 LGADELAYVFNGHRGQRWHLG-SEPFGRPWQPGDVVGCMIDLTENTIIFTLNGEVLMSDS 1172
Qy 1182 GGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRD 1240
Db 1173 GSETAFREIEIGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFAICGLQEGFEPFAINMQRP 1232
Qy 1241 VTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEK-ANWEFLRLS 1299
Db 1233 VTTWFSKGLPQFEPV-PLEHPHYEVSRVDGTVDTPPCLRLTHRTWGSQNSLVEMLFLRLS 1291
Qy 1300 LPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHY 1359
Db 1292 LPVQFHQHFRCTA----------GATPLAPPGL-- 1314
Qy 1360 EDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRST---SEAEMAKY 1416
Db 1315 ----------QPPAEDEARAAEPDPDYENLR--------RSAGGWSEAENGKE 1349
Qy 1417 DL---GAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGA 1473
Db 1350 GTAKEGAPGGTP----------QAGRGAPA-RAENEKDAT------TEKNKKRGF 1387
Qy 1474 RRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETV 1533
Db 1388 LFKAKKV----------AMMTQPP----------ATPTLPR-------LPHDVVPAD 1417
Qy 1534 GNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIIT 1593
Db 1418 NRD--DPEIILNTTTYYYSVRVFAGQEPSCVWAGWVTPDYHQHDMSFDLSKVRVVTVTMG 1475
Qy 1594 DDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGK 1653
Db 1476 DEQGNVHSSLKCSNCYMVWGGDF---VSPGQQGRISHTDLVIGCLVDLATGLMTFTANGK 1532
Qy 1654 DTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPR 1713
Db 1533 ESNTFFQVEPNTKLFPAVFVLPTHQNVIQFELGKQKNIMPLSAAMFQSERKNPAPQCPPR 1592
Qy 1714 LKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPI 1773
Db 1593 LEMQMLMPVSWSRMPNHFLQVETRRAGERLGWAVQCQEPLTMMALHIPEENRCMDILELS 1652
Qy 1774 EMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDL 1833
Db 1653 ERLDLQRFHSHTLRLYRAVCALGNNRVAHALCSHVDQAQLLHALEDAHLPGPLRAGYYDL 1712
Qy 1834 LIALHLESHATTMEACKNEFVIPLGPELKALYEEP-----DMGHSLRSLQ----TESVRP 1884
Db 1713 LISIHLESACRSRRSMLSEYIVPLTPETRAITLFPPGRSTENGHPRHGLPGVGVTTSLRP 1772
Qy 1885 QMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGS 1937
Db 1773 PHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHARDPVGAS 1832
Qy 1938 NENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGKDEHRK- 1989
Db 1833 VEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEDEEEGEEEDEEEKE 1892
Qy 1990 ----------GLLHMKMAEGAKLQMCYLLQHLNDIQLRH 2018
Db 1893 EDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFCDQELQH 1952
Qy 2019 RVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 1953 RVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQEQINMLLQFK 2012
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNI 2137
Db 2013 --DGTDEEDCPLPEEIRQDLLDFHQDLLAHCGIQL-----DGEEEEPEEETTLGSRLMSL 2065
Qy 2138 INTVK-------ELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMF 2190
Db 2066 LEKVRLVKKKEEKPEEERSAEESKPRSLQE-----LVSHMVVRWAQEDFVQSPELVRAMF 2120
Qy 2191 SLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKR 2250
Db 2121 SLLHRQYDGLGELLRALPRAYTISPSSVEDTMSLLECLGQIRSLLIVQMGPQEENLMIQS 2180
Qy 2251 LWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDT 2310
Db 2181 IGNIMNNKVFYQHPNLMRALGMHETVMEVMVNVLG----------GGESKE-IR 2223
Qy 2311 SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2370
Db 2224 FPKMVTSCCRFLCYFCRISRQNQRSMFDHLSYLLENSGIGL---GMQGSTPLDVAAASVI 2280
Qy 2371 ENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWV 2430
Db 2281 DNNELALALQEQDLEKVVSYLAGCGLQSCPMLVAKGYPDIGWKPCGGERYLDFLRFAVFV 2340
Qy 2431 NGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA--------DR 2481
Db 2341 NGESVEENANVVVRLLIRKPECFGPALRGEGGSGLLAAIEEAIRISEDPARDGPGIRRDR 2400
Qy 2482 RKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKN 2541
Db 2401 RR----EHFG---------EEPPEENRVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKG 2447
Qy 2542 ESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGL 2597
Db 2448 EALRIRAILRSLVPLEDLVGIISL--PLQIPTLGKDGALVQPK--MSASFVPDHKASMVL 2503
Qy 2598 FLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIK 2657

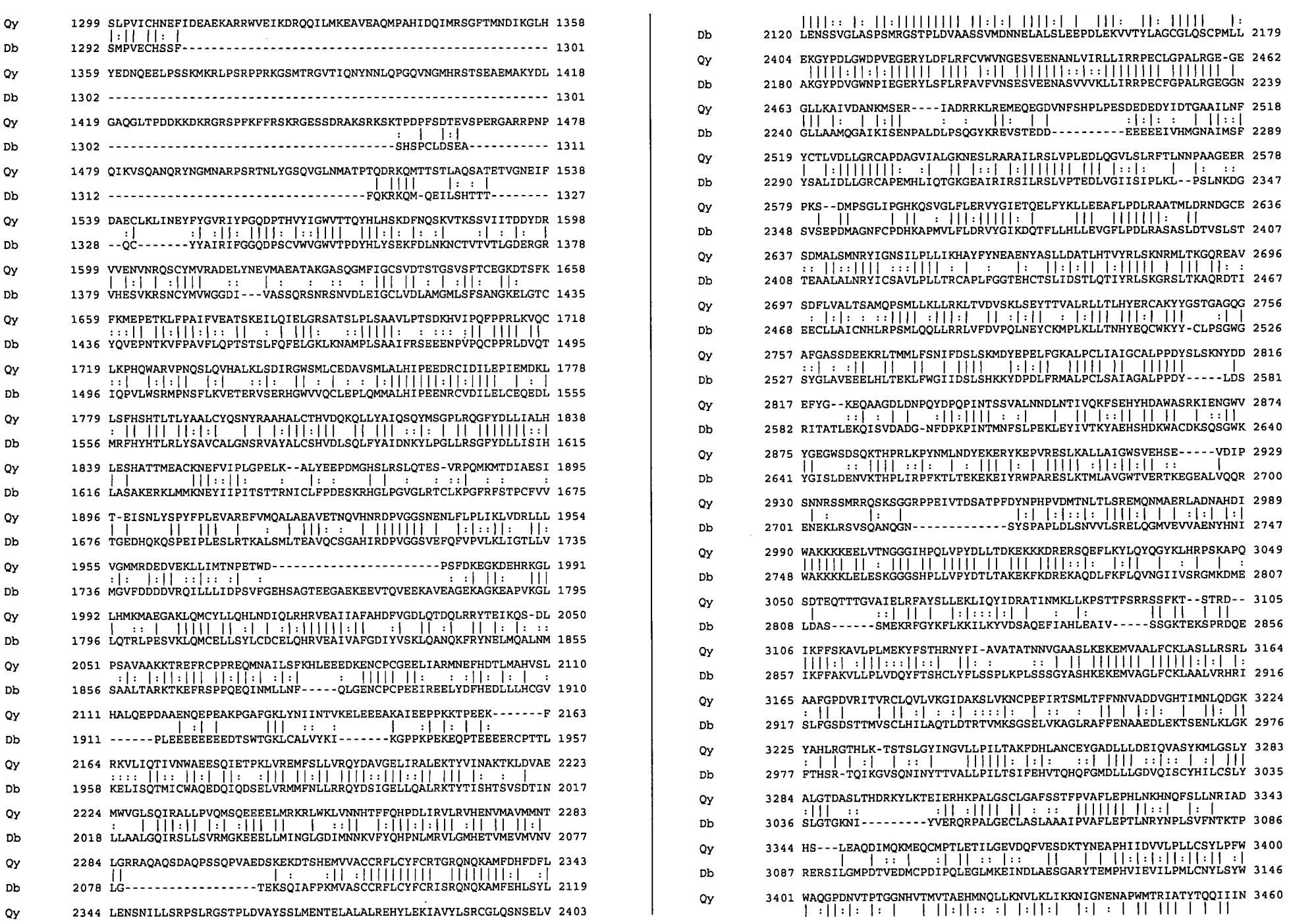

Db 2504 FLDRVYGIENQDFLLHVLDVGFLPDMRAAASLDTATFSTTEMALAVNRYLCLAVLPLITK 2563
Qy 2658 HAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLR 2717
Db 2564 CAPLFAGTEHRAIMVDSMLHTVYRLSRGRSLTKAQRDVIEDCLMSLCRYIRPSMLQHLLR 2623
Qy 2718 KLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIF 2777
Db 2624 RLVFDVPILNEFAKMPLKLLTNHYERCWKYY-CLPTGWANFGVTSEEELHLTRKLFWGIF 2682
Qy 2778 DSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQ 2836
Db 2683 DSLAHKKYDPELYRMAMPCLCAIAGALPPDY-----VDASYSSKAEKKATVDAEGNFDPR 2737
Qy 2837 PINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLN 2896
Db 2738 PVETLNVIIPEKLDSFINKFAEYTHEKWAFDKIQNNWSYGENIDEELKTHPMLRPYKTFS 2797
Qy 2897 DYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATP 2956
Db 2798 EKDKEIYRWPIKESLKAMIAWEWTIE----------KAREGEEEKTEKKKTAKISQSAQT 2847
Qy 2957 FD----YNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPY 3012
Db 2848 YDPREGYNPQPPDLSAVTLSRELQAMAEQLAENYHNTWGRKKKQELEAKGGGTHPLLVPY 2907
Qy 3013 DLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYSLLEK 3072
Db 2908 DTLTAKEKARDREKAQELLKFLQMNGYAVTRGLKDMELDSS------SIEKRFAFGFLQQ 2961
Qy 3073 LIQYIDRATINMKLLK--PSTTFSRRSSFKTSTRDIKFFSKAVLPLMEKYFSTHRNYFIA 3130
Db 2962 LLRWMD---ISQEFIAHLEAVVSSGRVEKSPHEQEIKFFAKILLPLINQYFTNHCLYFLS 3018
Qy 3131 V-ATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKS 3189
Db 3019 TPAKVLGSGGHASNKEKEMITSLFCKLAALVRHRVSLFGTDAPAVVNCLHILARSLDART 3078
Qy 3190 LVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLGYINGVLLPI 3249
Db 3079 VMKSGPEIVKAGLRSFFESASEDIEKMVENLRLGKVSQARTQVKGVGQNLTYTTVALLPV 3138
Qy 3250 LTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKTEIERHKPAL 3309
Db 3139 LTTLFQHIAQHQFGDDVILDDVQVSCYRTLCSIYSLGTTKN---------TYVEKLRPAL 3189
Qy 3310 GSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHS---LEAQDIMQKMEQCMPTLETIL 3366
Db 3190 GECLARLAAAMPVAFLEPQLNEYNACSVYTTKSPRERAILGLPNSVEEMCPDIPVLERLM 3249
Qy 3367 GEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPD---NVTPTGG-NHVTMVTAE 3422
Db 3250 ADIGGLAESGARYTEMPHVIEITLPMLCSYLPRWWERGPEAPPSALPAGAPPPCTAVTSD 3309
Qy 3423 HMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRKRTD 3482
Db 3310 HLNSLLGNILRIIVNNLGIDEASWMKRLAVFAQPIVSRARPELLQSHFIPTIGRLRKRAG 3369
Qy 3483 NMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWLRNN 3542
Db 3370 KVVSEEEQLALEAKA---EAQEGELLVRDEFSVLCRDLYALYPLLIRYVDNNRAQWLTEP 3426
Qy 3543 VPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDGTPQ 3602
Db 3427 NPSAEELFRMVGEIFIYWSKSHNFKREEQNFVVQNEINNMSFL--TADNK-----SKMAK 3479
Qy 3603 GGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMS 3662
Db 3480 SGGSDQERTKKKRRGDRYSVQTSLIVATLKKMLPIGLNMCAPTDQDLITLAKTRYALKDT 3539
Qy 3663 EQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKIIDDTVER 3722
Db 3540 DEEVREFLHNNLHLQGKVEGSPSLRWQMALYRGVPGRE------EDADDPEKI----VRR 3589
Qy 3723 IVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFAR 3782
Db 3590 VQEVSAVLYYLDQTEHPYKSKKAVWHKLLSKQRRRAVVACFRMTPLYNLPTHRACNMFLE 3649
Qy 3783 TYYELW-LEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTE 3841
Db 3650 SYKAAWILTEDHSFEDRMIDDLSKAGEQEE--EEEEVEE-KKPDPLHQLVLHFSRTALTE 3706
Qy 3842 RSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKL 3901
Db 3707 KS-KLDEDYLYMAYADIMAKSC---------HLEEGGENGEAEEEVEVSFEEKQMEKQRL 3756
Qy 3902 LFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKDK 3961
Db 3757 LYQQARLHTRGAAEMVLQMISACKGETGAMVSSTLKLGISILNGGNAEVQQKMLDYLKDK 3816
Qy 3962 KDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLG-VGLEGAA-----GEKNMHDAEFTCA 4015
Db 3817 KEVGFFQSIQALMQTCSVLDLNAFERQNKAEGLGMVNEDGTVINRQNGEKVMADDEFTQD 3876
Qy 4016 LFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELI 4075
Db 3877 LFRFLQLLCEGHNNDFQNYLRTQTGNTTTINIIICTVDYLLRLQESISDFYWYYSGKDVI 3936
Qy 4076 DPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKL 4135
Db 3937 EEQGKRNFSKAMSVAKQVFNSLTEYIQGPCTGNQQSLAHSRLWDAVVGFLHVFAHMMMKL 3996
Qy 4136 SKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFD 4195
Db 3997 AQDSSQIELLKELLDLQKDMVVMLLSLLEGNVVNGMIARQMVDMLVESSSNVEMILKFFD 4056
Qy 4196 MFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKL 4255
Db 4057 MFLKLKDIVGSEAFQDYVTDPRGLISKKDFQKAMDSQKQFSGPEIQFLLSCSEADENEMI 4116
Qy 4256 DYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEI 4315
Db 4117 NCEEFANRFQEPARDIGFNVAVLLTNLSEHVPHDPRLHNFLELAESILEYFRPYLGRIEI 4176
Qy 4316 MGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIF 4375
Db 4177 MGASRRIERIYFEISETNRAQWEMPQVKESKRQFIFDVVNEGGEAEKMELFVSFCEDTIF 4236
Qy 4376 EMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVA------ 4429
Db 4237 EMQIAAQISEPEGEP-------------ETDEDEGAG--AAEAGAEGAEEGAAGLEGTA 4280
Qy 4430 ----------------TAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYG 4473
Db 4281 ATAAAGATARVVAAAGRALRGLSYRSLRRRVRRLRRLTAREAATAVAALLWAAVTRAGAA 4340
Qy 4474 VLVVVRYIFGVLLGLMRGPQTDEPP-----------PEPTEEEKIGQLRHRLLATQSSR 4521
Db 4341 GAGAAAGALGLLWGSLFGGGLVEGAKKVTVTELLAGMPDPTSDEVHGE----------- 4388
Qy 4522 HLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHES---------- 4559
Db 4389 -QPAGPGGDADG--EGASEGAGDAAEGAGDEEEAVHEAGPGGADGAVAVTDGGPFRPEGA 4445
Qy 4560 -----PSTSTPSSGEEAEVSP----DESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQ 4610
Db 4446 GGLGDMGDTTPAEPPTPEGSPILKRKLGVDGVEEELPPE----PEPEPEPELEPEKADAE 4501
Qy 4611 AAQQAAMSAIEAESKKAVQGPAPSALSQV-------DLSQYTRRAVSFLARNFYNLKYVA 4663
Db 4502 NGEKEEVPEPTPEPPKKQAPPSPPPKKEEAGGEFWGELEVQRVKFLNYLSRNFYTLRFLA 4561
Qy 4664 LVLAFCINFVLLFYKVSTLDGEGG----EGSGLGDIIAGGGSGSGAGSGSGDGSGESGED 4719
Db 4562 LFLAFAINFILLFYKVS--DSPPGEDDMEGSAAGDV---SGAGSGGSSGWGLGAGEEAEG 4616

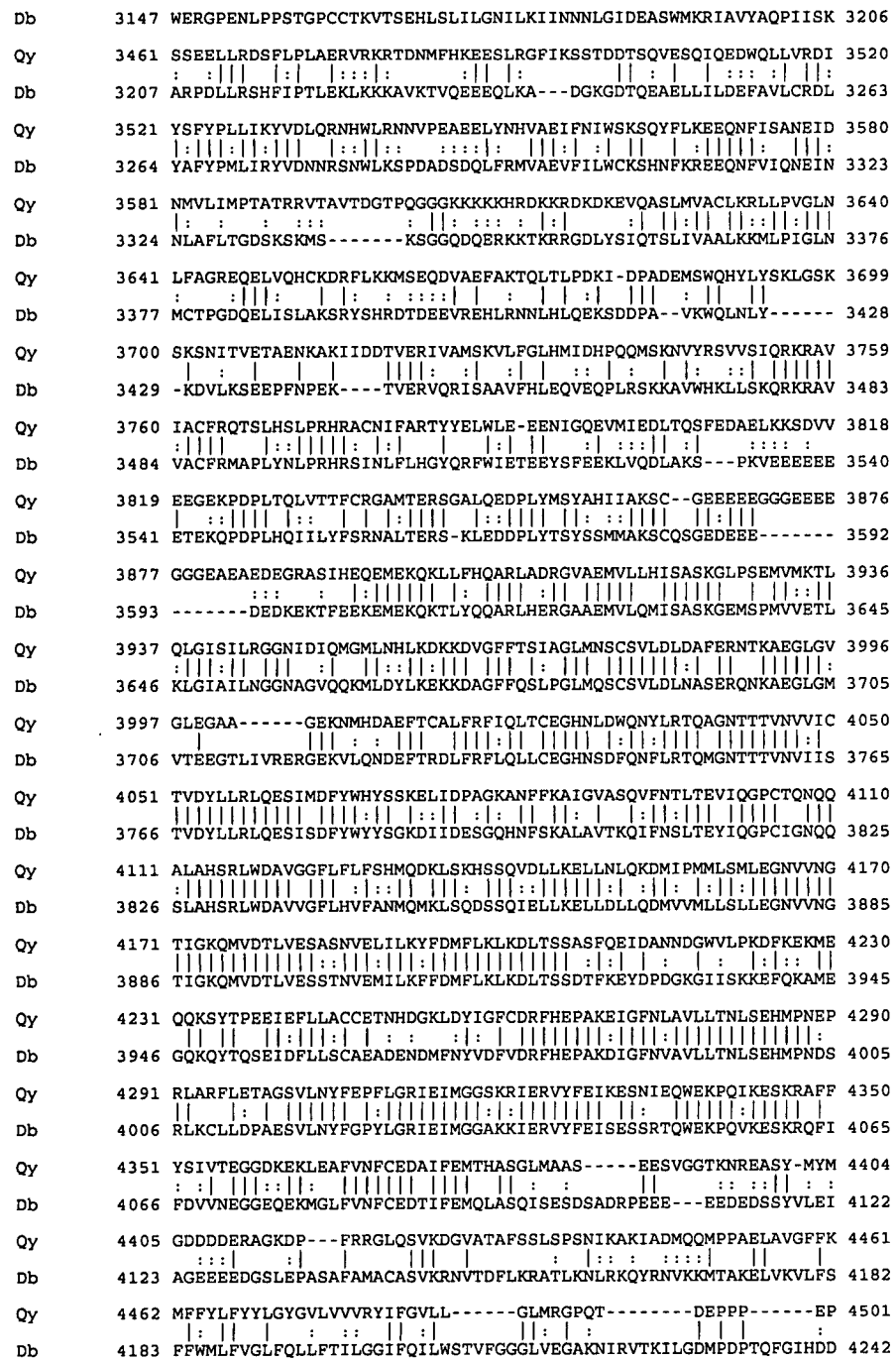
```
Qy       4720 DDALEVVH--IDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKL 4777
Db       4617 DEDENMVYYFLEESTGYMEPALRCLSLLHTLVAFLCIIGYNCLKVPLVIFKREKELARKL 4676

Qy       4778 EFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNML 4837
Db       4677 EFDGLYITEQPEDDDVKGQWDRLVLNTPSFPSNYWDKFVKRKVLDKHGDIYGRERIAELL 4736

Qy       4838 GM-----EKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVM 4892
Db       4737 GMDLATLEITAHNERKPNPPPGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLGWYMVMSLL 4796

Qy       4893 GNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRK 4952
Db       4797 GHYNNFFFAAHLLDIAMGVKTLRTILSSVTHNGKQLVMTVGLLAVVVYLYTVVAFNFFRK 4856

Qy       4953 FYVQEED-DEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFF 5011
Db       4857 FYNKSEDEDEPDMKCDDMMTCYLFHMYVGVRAGGGIGDEIEDPAGDEYELYRVVFDITFF 4916

Qy       5012 FFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQR 5071
Db       4917 FFVIVILLAIIQGLIIDAFGELRDQQEQVKEDMETKCFICGIGSDYFDTTPHGFETHTLE 4976

Qy       5072 EHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYED 5124
Db       4977 EHNLANYMFFLMYLINKDETEHTGQESYVWKMYQERCWDFFPAGDCFRKQYED 5029
```

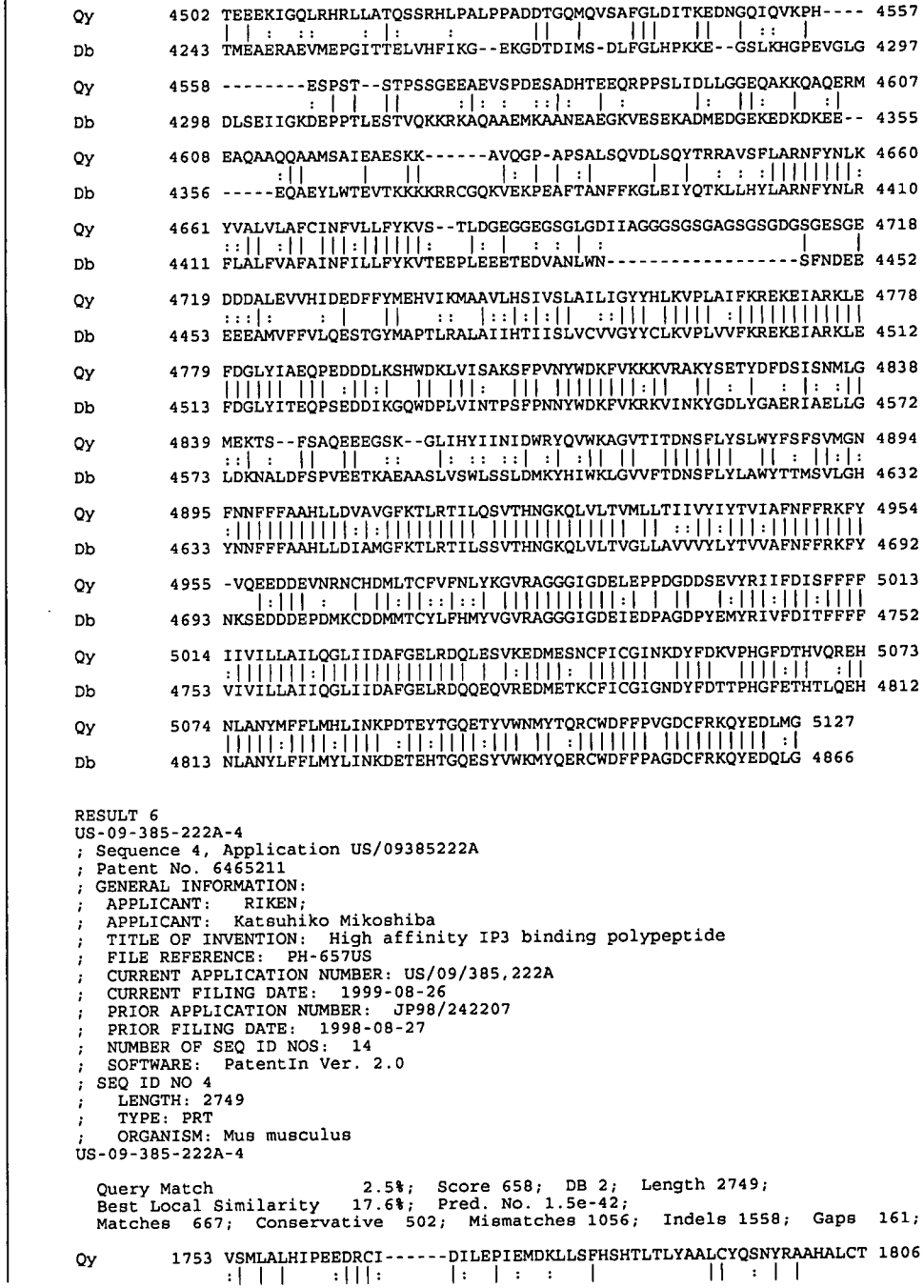
RESULT 5
US-09-424-783-2
; Sequence 2, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-783-2

Query Match 42.1%; Score 11295.5; DB 2; Length 4866;
Best Local Similarity 44.6%; Pred. No. 0;
Matches 2350; Conservative 908; Mismatches 1457; Indels 559; Gaps 93;

```
Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIATIHKEQRKFCLAAEGLGNRLCFLEPTSEAKYIPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAVLLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        122 CLTTSRSQTDKLAFDVGLREHATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
Db        182 LHLSVSNGNIQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        240 DQNDSQHRRIFYEAGGAGTRARSLWRVEPLRISWSGSNIRWGQAFRLRHLTTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLED---KDLEVIGAPIIKYGDSTVIVQHS 352
Db        300 DQGLILQDRAKSDTKSTAFSFRASK-ELKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHI 358

Qy        353 ETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSL 412
Db        359 ASGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTAL 417

Qy        413 FTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
Db        418 FSQFVSG-----NNRTAAPI--TLPIEEVLQTLQDLIAYFQPPEEEMRHEDKQNKLRSLK 470

Qy        473 NRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIK 532
Db        471 NRQNLFKEEGMLALVLNCIDRLNVYNSVAHFAG-IAREESGMAWKEILNLLYKLLAALIR 529

Qy        533 GNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVII 592
Db        530 GNRNNCAQF--SNNLDWLISKLDRLES--SSGILEVLHCILTESPEALNLIAEGHIKSII 585

Qy        593 SLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPN 652
Db        586 SLLDKHGRNHKVLDILCSLCLCNGVAVRANQNLICDNLLPRRNLLLQTRLINDVTSIRPN 645

Qy        653 IFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGV 711
Db        646 IFLGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASSSGYAPYPGGGEGWGGNGV 705

Qy        712 GDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDV-------IGCALDLTVPIINFM 764
Db        706 GDDLYSYGFDGLHLWSG--RIPRAVASINQHLLRSDDVGKLLPGPRGC------PASHSA 757

Qy        765 FNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQ 824
Db        758 SMGSPCRGCLENFNTDGLFFPVMSFSAGVKVRFLMGGRHGEFKFLPPSGYAPCYEALLPK 817

Qy        825 QILSLEPCFYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENI 882
Db        818 EKMRLEPVKEYKRDADGIRDLLGTTQFLSQASFIPCPVDTSQVILPPHLEKIRDRLAENI 877

Qy        883 HEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYY 942
Db        878 HELWGMNKIELGWTFGKIRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLTLGCH 937

Qy        943 ISLDKPPAR--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWA 1000
Db        938 IAHVNPAAEEDLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWA 996

Qy       1001 RERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPT 1060
Db        997 KDRIKQGWTYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFVGYGYNIEPSD 1056

Qy       1061 GEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGM 1120
Db       1057 QELADSAVEKVSIDK---IRFFRVERSYPVRSGKWYFEFEVVTGGDMRVGWARPGCRPDV 1113

Qy       1121 MLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDA 1180
Db       1114 ELGADDQAFVFEGNRGQRWHQG-SGYFGRTWQPGDVVGCMINLDDASMIFTLNGELLITN 1172

Qy       1181 LGGETTFADVQGDN-FVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKR 1239
Db       1173 KGSELAFADYEIENGFVPICCLGLSQIGRMNLGTDASTFKFYTMCGLQEGFEPFAVNMNR 1232

Qy       1240 DVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETM-EKANWEFLRL 1298
Db       1233 DVAMWFSKRLPTFVNVPK-DHPHIEVMRIDGTMDSPPCLKVTHKTFGTQNSNADMIYCRL 1291
```

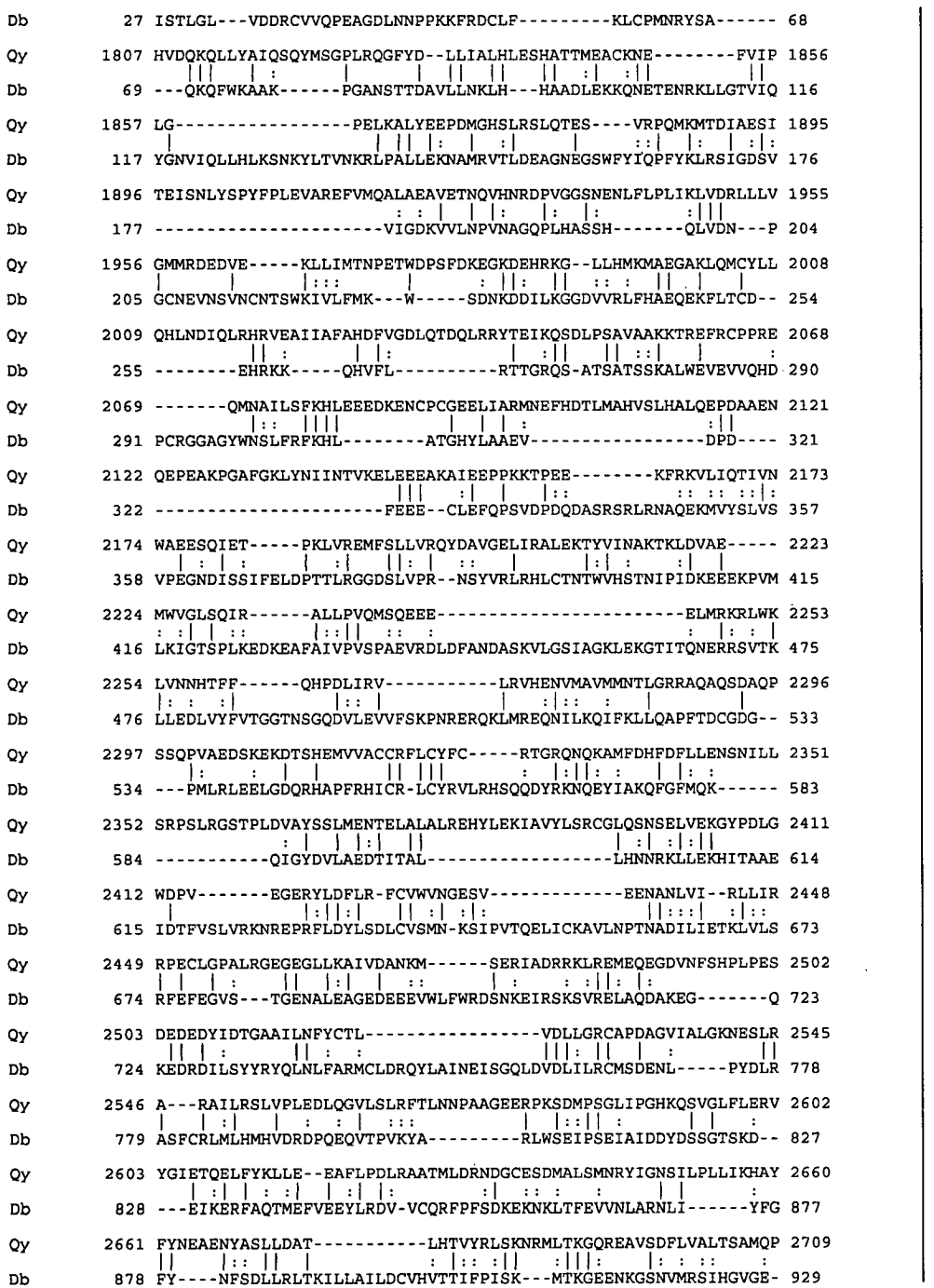






RESULT 6
US-09-385-222A-4
; Sequence 4, Application US/09385222A
; Patent No. 6465211
; GENERAL INFORMATION:
; APPLICANT: RIKEN;
; APPLICANT: Katsuhiko Mikoshiba
; TITLE OF INVENTION: High affinity IP3 binding polypeptide
; FILE REFERENCE: PH-657US
; CURRENT APPLICATION NUMBER: US/09/385,222A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: JP98/242207
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2749
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-385-222A-4

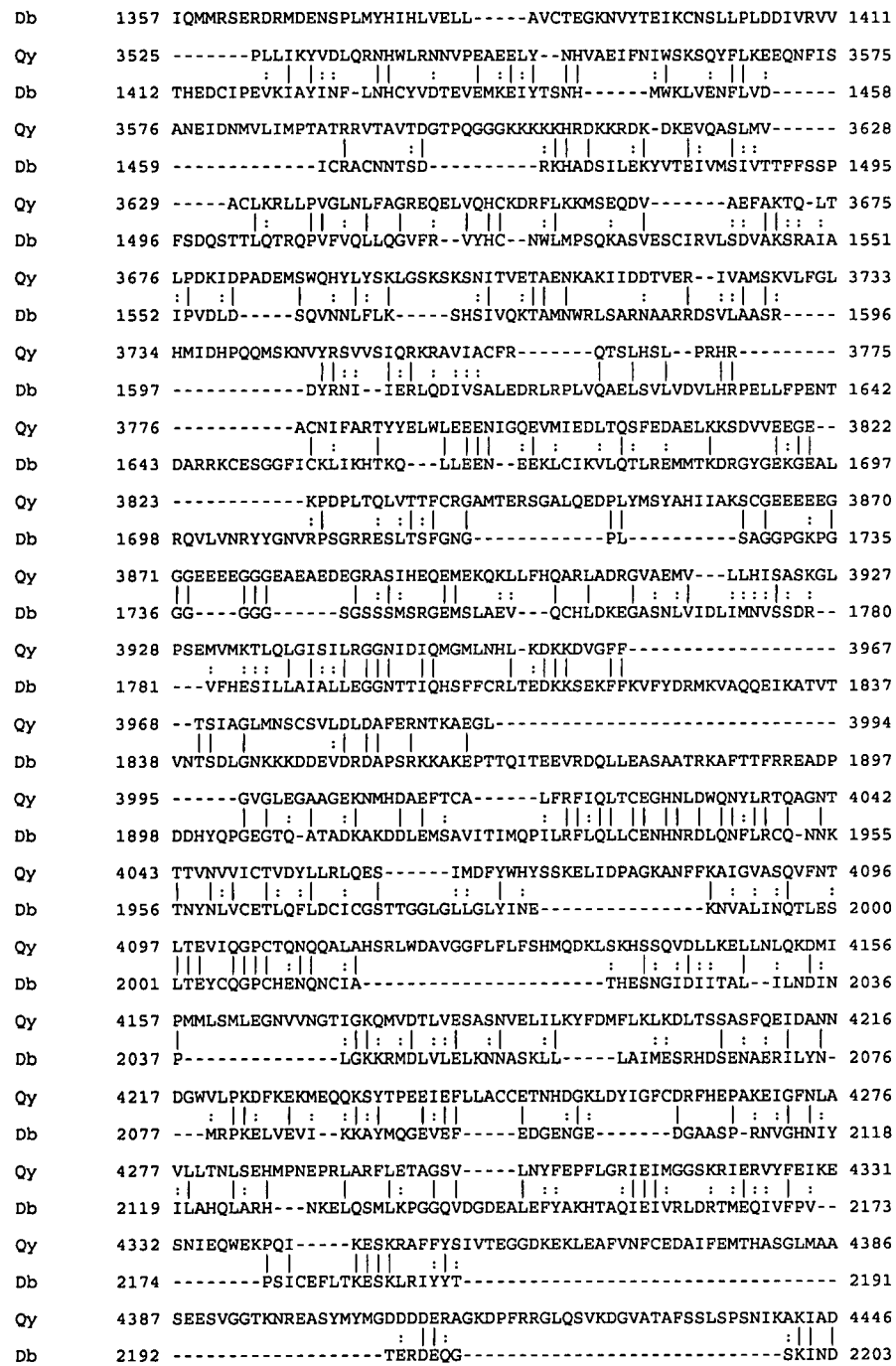
Query Match 2.5%; Score 658; DB 2; Length 2749;
Best Local Similarity 17.6%; Pred. No. 1.5e-42;
Matches 667; Conservative 502; Mismatches 1056; Indels 1558; Gaps 161;

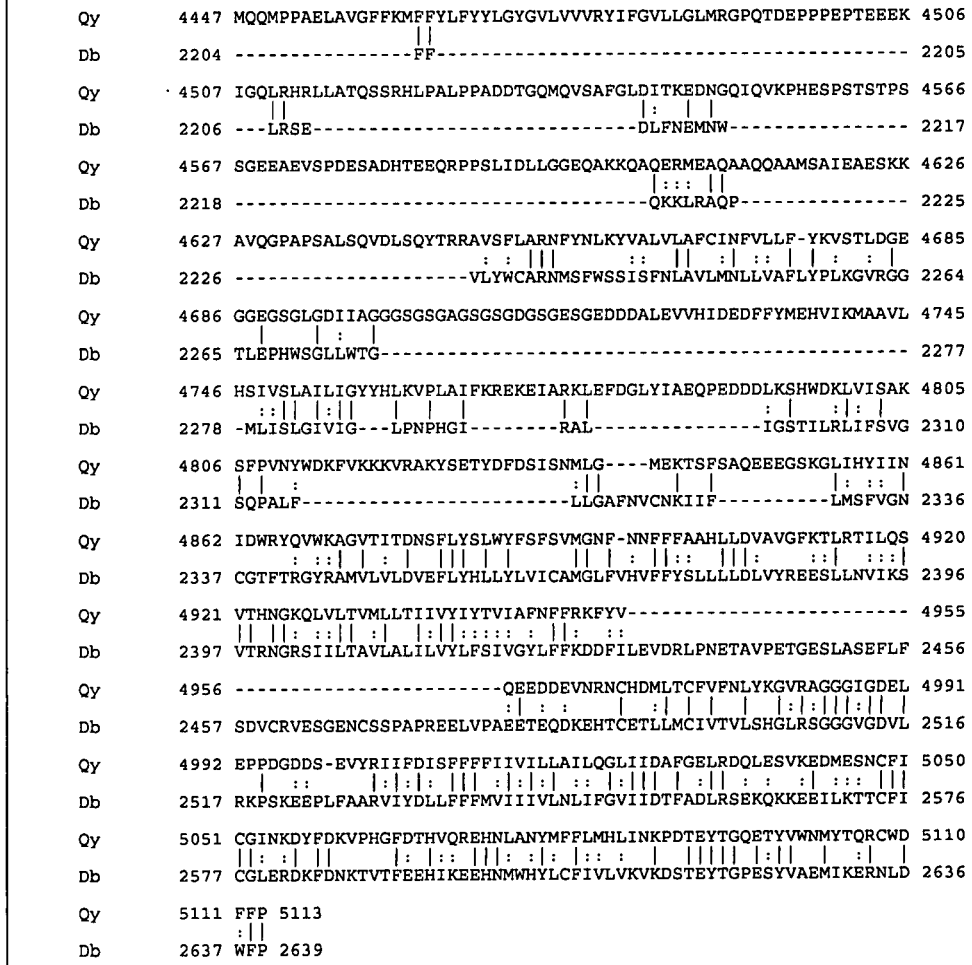

Db 27 ISTLGL---VDDRCVVQPEAGDLNNPPKKFRDCLF---------KLCPMNRYSA------ 68
Qy 1807 HVDQKQLLYAIQSQYMSGPLRQGFYD--LLIALHLESHATTMEACKNE--------FVIP 1856
Db 69 ---QKQFWKAAK------PGANSTTDAVLLNKLH---HAADLEKKQNETENRKLLGTVIQ 116
Qy 1857 LG----------PELKALYEEPDMGHSLRSLQTES----VRPQMKMTDIAESI 1895
Db 117 YGNVIQLLHLKSNKYLTVNKRLPALLEKNAMRVTLDEAGNEGSWFYIQPFYKLRSIGDSV 176
Qy 1896 TEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLV 1955
Db 177 ----------VIGDKVVLNPVNAGQPLHASSH-------QLVDN---P 204
Qy 1956 GMMRDEDVE-----KLLIMTNPETWDPSFDKEGKDEHRKG--LLHMKMAEGAKLQMCYLL 2008
Db 205 GCNEVNSVNCNTSWKIVLFMK---W-----SDNKDDILKGGDVVRLFHAEQEKFLTCD-- 254
Qy 2009 QHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPRE 2068
Db 255 --------EHRKK-----QHVFL----------RTTGRQS-ATSATSSKALWEVEVVQHD 290
Qy 2069 -------QMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAEN 2121
Db 291 PCRGGAGYWNSLFRFKHL--------ATGHYLAAEV----------DPD---- 321
Qy 2122 QEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEE--------KFRKVLIQTIVN 2173
Db 322 ----------FEEE--CLEFQPSVDPDQDASRSRLRNAQEKMVYSLVS 357
Qy 2174 WAEESQIET-----PKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAE----- 2223
Db 358 VPEGNDISSIFELDPTTLRGGDSLVPR--NSYVRLRHLCTNTWVHSTNIPIDKEEEKPVM 415
Qy 2224 MWVGLSQIR------ALLPVQMSQEEE----------ELMRKRLWK 2253
Db 416 LKIGTSPLKEDKEAFAIVPVSPAEVRDLDFANDASKVLGSIAGKLEKGTITQNERRSVTK 475
Qy 2254 LVNNHTFF------QHPDLIRV----------LRVHENVMAVMMNTLGRRAQAQSDAQP 2296
Db 476 LLEDLVYFVTGGTNSGQDVLEVVFSKPNRERQKLMREQNILKQIFKLLQAPFTDCGDG-- 533
Qy 2297 SSQPVAEDSKEKDTSHEMVVACCRFLCYFC-----RTGRQNQKAMFDHFDFLLENSNILL 2351
Db 534 ---PMLRLEELGDQRHAPFRHICR-LCYRVLRHSQQDYRKNQEYIAKQFGFMQK------ 583
Qy 2352 SRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLG 2411
Db 584 ----------QIGYDVLAEDTITAL----------LHNNRKLLEKHITAAE 614
Qy 2412 WDPV-------EGERYLDFLR-FCVWVNGESV----------EENANLVI--RLLIR 2448
Db 615 IDTFVSLVRKNREPRFLDYLSDLCVSMN-KSIPVTQELICKAVLNPTNADILIETKLVLS 673
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKM------SERIADRRKLREMEQEGDVNFSHPLPES 2502
Db 674 RFEFEGVS---TGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEG-------Q 723
Qy 2503 DEDEDYIDTGAAILNFYCTL----------VDLLGRCAPDAGVIALGKNESLR 2545
Db 724 KEDRDILSYYRYQLNLFARMCLDRQYLAINEISGQLDVDLILRCMSDENL-----PYDLR 778
Qy 2546 A---RAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERV 2602
Db 779 ASFCRLMLHMHVDRDPQEQVTPVKYA---------RLWSEIPSEIAIDDYDSSGTSKD-- 827
Qy 2603 YGIETQELFYKLLE--EAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAY 2660
Db 828 ---EIKERFAQTMEFVEEYLRDV-VCQRFPFSDKEKNKLTFEVVNLARNLI------YFG 877
Qy 2661 FYNEAENYASLLDAT----------LHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQP 2709
Db 878 FY----NFSDLLRLTKILLAILDCVHVTTIFPISK---MTKGEENKGSNVMRSIHGVGE- 929
Qy 2710 SMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQG-AFGASSDEEKRL 2768
Db 930 -----LMTQVVLRGGGFLPMTPMA----------AAPEGNVKQAEPEKEDIM 966
Qy 2769 TMMLFSNIFDSLS-----KMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQ 2823
Db 967 VMDTKLKIIEILQFILNVRLDYR-------ISCLLCI---------FKREFDES------ 1004
Qy 2824 AAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQ 2883
Db 1005 ----------NSQSSETSS----------GNSS 1017
Qy 2884 KTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSG 2943
Db 1018 QEGPSNVPGAL--DFEH------IEEQAEGI--FGGSEENTPLDLDDH----------G 1056
Qy 2944 GRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGG 3003
Db 1057 GRTFLRVLLHLTMHDYPP--------LVSGALQLLFRHFSQRQEVLQAFKQVQLLVTS-- 1106
Qy 3004 GIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSK-----APQSDTEQTTTG 3058
Db 1107 --------QDVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDEPMDGASGENEHKKTEEG 1158
Qy 3059 VAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLME 3118
Db 1159 TS----------KPLKHEST----SSY---------- 1171
Qy 3119 KYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCL 3178
Db 1172 -------NYRVV----------KEIL----------IRLSKLCV 1188
Qy 3179 QVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTS 3238
Db 1189 Q------ESASVRKS-----RKQQQRLLRNM----------GAH------ 1211
Qy 3239 LGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYL 3298
Db 1212 -----AVVLELLQIPY------EKAEDTKMQEIMRLAHEFLQNF---------- 1244
Qy 3299 KTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQC 3358
Db 1245 ----------CAGNQQNQ---ALLHKHINLFLKPGILEAVTMQHI----FMNNFQLC 1284
Qy 3359 MPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTM 3418
Db 1285 SEINERV---VQHFV----------HCIE----------THGRNVQY 1308
Qy 3419 VTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELL-----RDSFLPL 3473
Db 1309 I--KFLQTIVKAEGKFIKK----------CQDMVMAELVNSGEDVLVFYNDRASFQTL 1354
Qy 3474 AERVRKRTDNM---------FHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFY 3524
Db 1355 IQMMRSERDRMDENSPLMYHIHLVELL-----AVCTEGKNVYTEIKCNSLLPLDDIVRVV 1409
Qy 3525 -------PLLIKYVDLQRNHWLRNNVPEAEELY--NHVAEIFNIWSKSQYFLKEEQNFIS 3575
Db 1410 THEDCIPEVKIAYINF-LNHCYVDTEVEMKEIYTSNHMWKLF----------ENFL- 1454
Qy 3576 ANEIDNMVLIMPTATRRVTAVTDGTPQGGGKKKKKHRDKKRDK-DKEVQASLMV------ 3628
Db 1455 ---VD--------ICRACNNTSD----------RKHADSILEKYVTEIVMSIVTTFFSSP 1493
Qy 3629 -----ACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSEQDV-------AEFAKTQ-LT 3675
Db 1494 FSDQSTTLQTRQPVFVQLLQGVFR--VYHC--NWLMPSQKASVESCIRVLSDVAKSRAIA 1549
Qy 3676 LPDKID----------PADEMSWQHYLYSKLGSKSKSNIT--------VETAENKA 3713
Db 1550 IPVDLDSQVNNLFLKSHNIVQKTALNWR--LSARNAARRDSVLAASRDYRNIIERLQDIV 1607

```
Qy       3714 KIIDDTVERIV-AMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLP 3772
Db       1608 SALEDRLRPLVQAELSVL--VDVLHRPELL----FPENTDARRK-----CESGGFICKLI 1656

Qy       3773 RH----------RACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVE--- 3819
Db       1657 KHTKQLLEENEEKLCIKVLQTLREMMTKDRGYGEKQISID---ESENAELPQAPEAENST 1713

Qy       3820 --EGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEE--------- 3868
Db       1714 EQELEPSPPLRQLED-------HKRGEALRQILVNRYYGNI--RPSGRRESLTSFGNGPL 1764

Qy       3869 EGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVL-LHISASKGL 3927
Db       1765 SPGGPSKPGGG---GGGPGSSSTSRGEMSLAEV---QCHLDKEGASNLVIDLIMNASS-- 1816

Qy       3928 PSEMVMKTLQLGISILRGGNIDIQMGMLNHL-KDKKDVGFF------------------- 3967
Db       1817 -DRVFHESILLAIALLEGGNTTIQHSFFCRLTEDKKSEKFFKVFYDRMKVAQQEIKATVT 1875

Qy       3968 --TSIAGLMNSCSVLDLDAFERNTKAEGL------------------------------ 3994
Db       1876 VNTSDLGNKKKDDEVDRDAPSRKKAKEPTTQITEEVRDQLLEASAATRKAFTTFRREADP 1935

Qy       3995 ------GVGLEGAAGEKNMHDAEFTCA------LFRFIQLTCEGHNLDWQNYLRTQAGNT 4042
Db       1936 DDHYQSGEGTQ-ATTDKAKDDLEMSAVITIMQPILRFLQLLCENHNRDLQNFLRCQ-NNK 1993

Qy       4043 TTVNVVICTVDYLLRLQES------IMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNT 4096
Db       1994 TNYNLVCETLQFLDCICGSTTGGLGLLGLYINE--------------KNVALINQTLES 2038

Qy       4097 LTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMI 4156
Db       2039 LTEYCQGPCHENQNCIA---------------------THESNGIDIITAL--ILNDIN 2074

Qy       4157 PMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANN 4216
Db       2075 P-------------LGKKRMDLVLELKNNASKLL-----LAIMESRHDSENAERILYN- 2114

Qy       4217 DGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLA 4276
Db       2115 ---MRPKELVEVI--KKAYMQGEVEF-----EDGENGE-------DGAASP-RNVGHNIY 2156

Qy       4277 VLLTNLSEHMPNEPRLARFLETAGSV-----LNYFEPFLGRIEIMGGSKRIERVYFEIKE 4331
Db       2157 ILAHQLARH---NKELQTMLKPGGQVDGDEALEFYAKHTAQIEIVRLDRTMEQIVFPV-- 2211

Qy       4332 SNIEQWEKPQI-----KESKRAFFYSIVTEGGDK-EKLEAFVNFCEDAIFEMTHASGLMA 4385
Db       2212 --------PSICEFLTKESKLRIYYT--TERDEQGSKINDFFLRSEDLFNEMNWQKKLRA 2261

Qy       4386 ASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNIKAKIA 4445
Db       2262 ------------------------------------QPVLYWCARNMSFW--SSISFNLA 2283

Qy       4446 DMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEE 4505
Db       2284 VLMNLLVA---------FFYPFKGVRGGTL---------------------------- 2304

Qy       4506 KIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESPSTSTP 4565
Db       2305 ------------------------------------------------EPHWS------ 2309

Qy       4566 SSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESK 4625
Db       2310 ------------------------------------------------------------ 2309

Qy       4626 KAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGE 4685
Db       2310 -------------------------------GLLWTAMLISLAIVIAL----------- 2326

Qy       4686 GGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYMEHVIKMAAVL 4745
Db       2327 -PKPHGIRALIA-------------------------------------------STIL 2341

Qy       4746 HSIVSLAI-----LIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKL 4800
Db       2342 RLIFSVGLQPTLFLLGAFN-------------VCNKIIF---------------------- 2367

Qy       4801 VISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYII 4860
Db       2368 ------------------------------------------------------LMSFVG 2373

Qy       4861 NIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNF-NNFFFAAHLLDVAVGFKTLRTILQ 4919
Db       2374 NCGTFTRGYRA--MVLDVEFLYHLLYLLICAMGLFVHEFFYSLLLFDLVYREETLLNVIK 2431

Qy       4920 SVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYV---------------------- 4955
Db       2432 SVTRNGRSIILTAVLALILVYLFSIVGYLFFKDDFILEVDRLPNETAVPETGESLANDFL 2491

Qy       4956 ------------------------QEEDDEVNRNCHDMLTCFVFNLYKGVRAGGGIGDE 4990
Db       2492 YSDVCRVETGENCTSPAPKEELLPAEETEQDKEHTCETLLMCIVTVLSHGLRSGGGVGDV 2551

Qy       4991 LEPPDGDDS-EVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCF 5049
Db       2552 LRKPSKEEPLFAARVIYDLLFFFMVIIIVLNLIFGVIIDTFADLRSEKQKKEEILKTTCF 2611

Qy       5050 ICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCW 5109
Db       2612 ICGLERDKFDNKTVTFEEHIKEEHNMWHYLCFIVLVKVKDSTEYTGPESYVAEMIRERNL 2671

Qy       5110 DFF 5112
Db       2672 DWF 2674
```

```
RESULT 7
PCT-US96-01735-1
; Sequence 1, Application PC/TUS9601735
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, Andrew R.
;    TITLE OF INVENTION:  HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01735
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/386,039
;      FILING DATE:  09-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kole, Lisa B
;      REGISTRATION NUMBER:  35,225
;      REFERENCE/DOCKET NUMBER:  A30042 - 165/30555
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2628
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
```

```
;       LENGTH:  2713 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;     FEATURE:
PCT-US96-01735-1

  Query Match             2.4%;  Score 654;  DB 5;  Length 2713;
  Best Local Similarity   17.8%;  Pred. No. 3.1e-42;
  Matches  673;  Conservative  485;  Mismatches 1033;  Indels 1592;  Gaps  163;

Qy       1753 VSMLALHIPEEDRCI------DILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCT 1806
Db         27 ISTLGL---VDDRCVVQPETGDLNNPPKKFRDCLF---------KLCPMNRYSA------ 68
Qy       1807 HVDQKQLLYAIQSQYMSGPLRQGFYD--LLIALHLESHATTMEACKNE--------FVIP 1856
Db         69 ---QKQFWKAAK------PGANSTTDAVLLNKLH---HAADLEKKQNETENRKLLGTVIQ 116
Qy       1857 LG-----------------PELKALYEEPDMGHSLRSLQTES----VRPQMKMTDIAESI 1895
Db        117 YGNVIQLLHLKSNKYLTVNKRLPALLEKNAMRVTLDEAGNEGSWFYIQPFYKLRSIGDSV 176
Qy       1896 TEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLV 1955
Db        177 ---------------------VIGDKVVLNPVNAGQPLHASSH-------QLVDN---P 204
Qy       1956 GMMRDEDVE-----KLLIMTNPETWDPSFDKEGKDEHRKG--LLHMKMAEGAKLQMCYLL 2008
Db        205 GCNEVNSVNCNTSWKIVLFMK---W-----SDNKDDILKGGDVVRLFHAEQEKFLTCD-- 254
Qy       2009 QHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPRE 2068
Db        255 --------EHRKK-----QHVFL----------RTTGRQS-ATSATSSKALWEVEVVQHD 290
Qy       2069 -------QMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAEN 2121
Db        291 PCRGGAGYWNSLFRFKHL--------ATGHYLAAEV-----------------DPD---- 321
Qy       2122 QEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEE--------KFRKVLIQTIVN 2173
Db        322 ---------------------FEEE--CLEFQPSVDPDQDASRSRLRNAQEKMVYSLVS 357
Qy       2174 WAEESQIET-----PKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAE----- 2223
Db        358 VPEGNDISSIFELDPTTLRGGDSLVPR--NSYVRLRHLCTNTWVHSTNIPIDKEEEKPVM 415
Qy       2224 MWVGLSQIR------ALLPVQMSQEEE-----------------------ELMRKRLWK 2253
Db        416 LKIGTSPVKEDKEAFGIVPVSPAEVRDLDFANDASKVLGSIAGKLEKGTITQNERRSVTK 475
Qy       2254 LVNNHTFF------QHPDLIRV-----------LRVHENVMAVMMNTLGRRAQAQSDAQP 2296
Db        476 LLEDLVYFVTGGTNSGQDVLEVVFSKPNRERQKLMREQNILKQIFKLLQAPFTDCGDG-- 533
Qy       2297 SSQPVAEDSKEKDTSHEMVVACCRFLCYFC-----RTGRQNQKAMFDHFDFLLENSNILL 2351
Db        534 ---PMLRLEELGDQRHAPFRHICR-LCYRVLRHSQQDYRKNQEYIAKQFGFMQK------ 583
Qy       2352 SRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLG 2411
Db        584 -----------QIGYDVLAEDTITAL-----------------LHNNRKLLEKHITAAE 614
Qy       2412 WDPV-------EGERYLDFLR-FCVWVNGESV-------------EENANLVI--RLLIR 2448
Db        615 IDTFVSLVRKNREPRFLDYLSDLCVSMN-KSIPVTQELICKAVLNPTNADILIETKLVLS 673
Qy       2449 RPECLGPALRGEGEGLLKAIVDANKM------SERIADRRKLREMEQEGDVNFSHPLPES 2502
Db        674 RFEFEG--VSSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQDAKEG-------Q 724
Qy       2503 DEDEDYIDTGAAILNFYCTL----------------VDLLGRCAPDAGVIALGKNESLR 2545
Db        725 KEDRDVLSYYRYQLNLFARMCLDRQYLAINEISGQLDVDLILRCMSDENL-----PYDLR 779
Qy       2546 A---RAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERV 2602
Db        780 ASFCRLMLHMHVDRDPQEQVTPVKYA---------RLWSEIPSEIAIDDYDSSGASKD-- 828
Qy       2603 YGIETQELFYKLLE--EAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAY 2660
Db        829 ---EIKERFAQTMEFVEEYLRDV-VCQRFPFSDKEKNKLTFEVVNLARNLI------YFG 878
Qy       2661 FYNEAENYASLLDAT-----------LHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQP 2709
Db        879 FY----NFSDLLRLTKILLAILDCVHVTTIFPISK---MAKGEENKGSNVMRSIHGVGE- 930
Qy       2710 SMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQG-AFGASSDEEKRL 2768
Db        931 -----LMTQVVLRGGGFLPMTPMA------------------AAPEGNVKQAEPEKEDIM 967
Qy       2769 TMMLFSNIFDSLS-----KMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQ 2823
Db        968 VMDTKLKIIEILQFILNVRLDYR-------ISCLLCI-------------FKREFWMKA- 1006
Qy       2824 AAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQ 2883
Db       1007 ----------IPRTSETSS------------------------------------GNSS 1019
Qy       2884 KTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSG 2943
Db       1020 QEGPSNVPGAL--DFEH------IEEQAEGI--FGGSEENTPLDLDDH-----------G 1058
Qy       2944 GRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGG 3003
Db       1059 GRTFLRVLLHLTMHDYPP--------LVSGALQLLFRHFSQRQEVLQAFKQVQLLVTS-- 1108
Qy       3004 GIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSK-----APQSDTEQTTTG 3058
Db       1109 --------QDVDNYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKKTEEG 1160
Qy       3059 VAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLME 3118
Db       1161 -----------------------NNKPQKHEST----SSY------------------ 1173
Qy       3119 KYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCL 3178
Db       1174 -------NYRVV---------------KEIL--------------------IRLSKLCV 1190
Qy       3179 QVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTS 3238
Db       1191 Q------ESASVRKS-----RKQQQRLLRNM--------------------GAH------ 1213
Qy       3239 LGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYL 3298
Db       1214 -----AVVLELLQIPY------EKAEDTKMQEIMRLAHEFLQNF--------------- 1246
Qy       3299 KTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQC 3358
Db       1247 -------------CAGNQQNQ---ALLHKHINLFLNPGILEAVTMQHI----FMNNFQLC 1286
Qy       3359 MPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTM 3418
Db       1287 SEINERV---VQHFV----------HCIE---------------------THGRNVQY 1310
Qy       3419 VTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELL-----RDSFLPL 3473
Db       1311 I--KFLQTIVKAEGKFIKK-----------CQDMVMAELVNSGEDVLVFYNDRASFQTL 1356
Qy       3474 AERVRKRTDNM---------FHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFY 3524
```



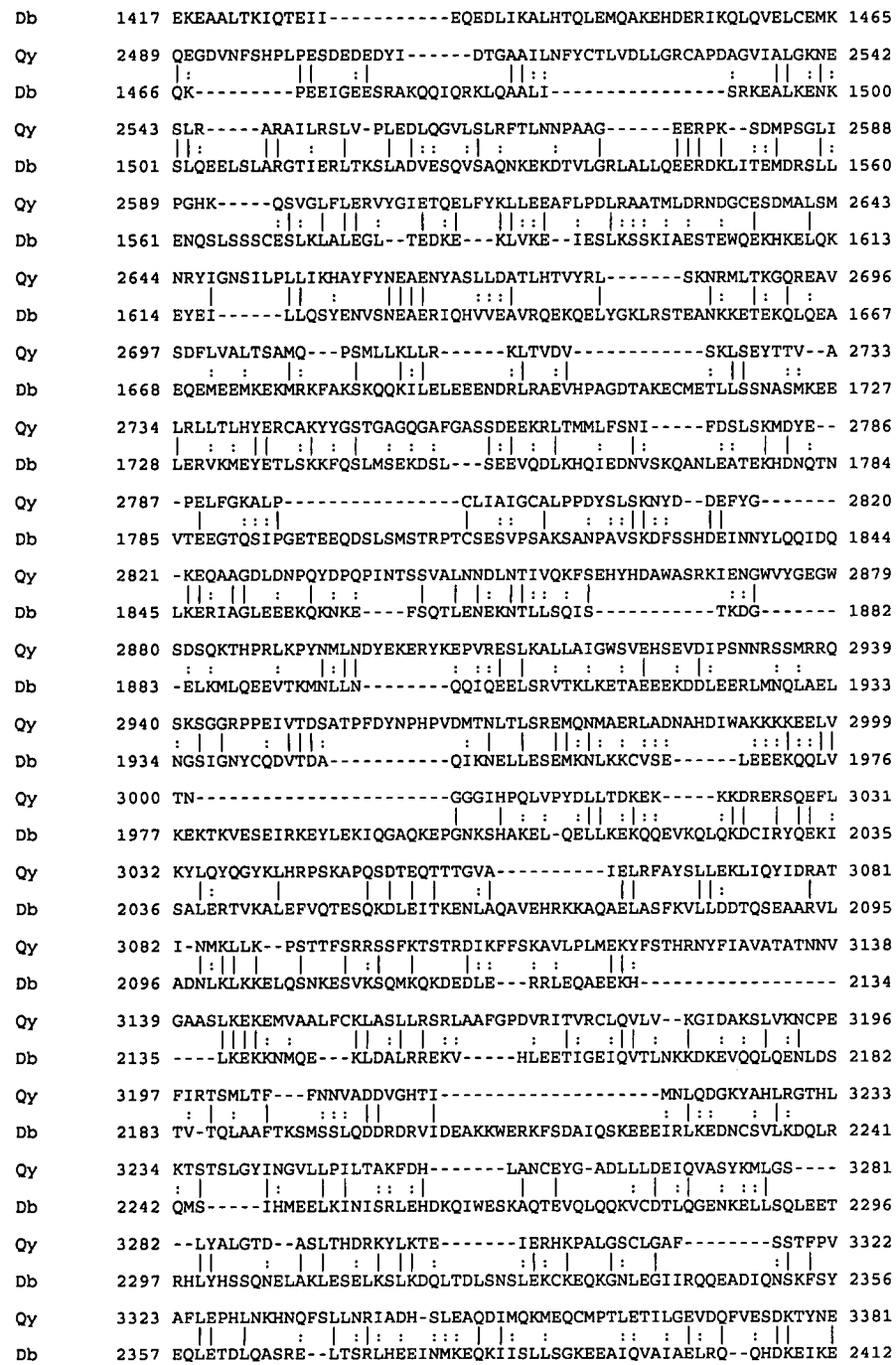


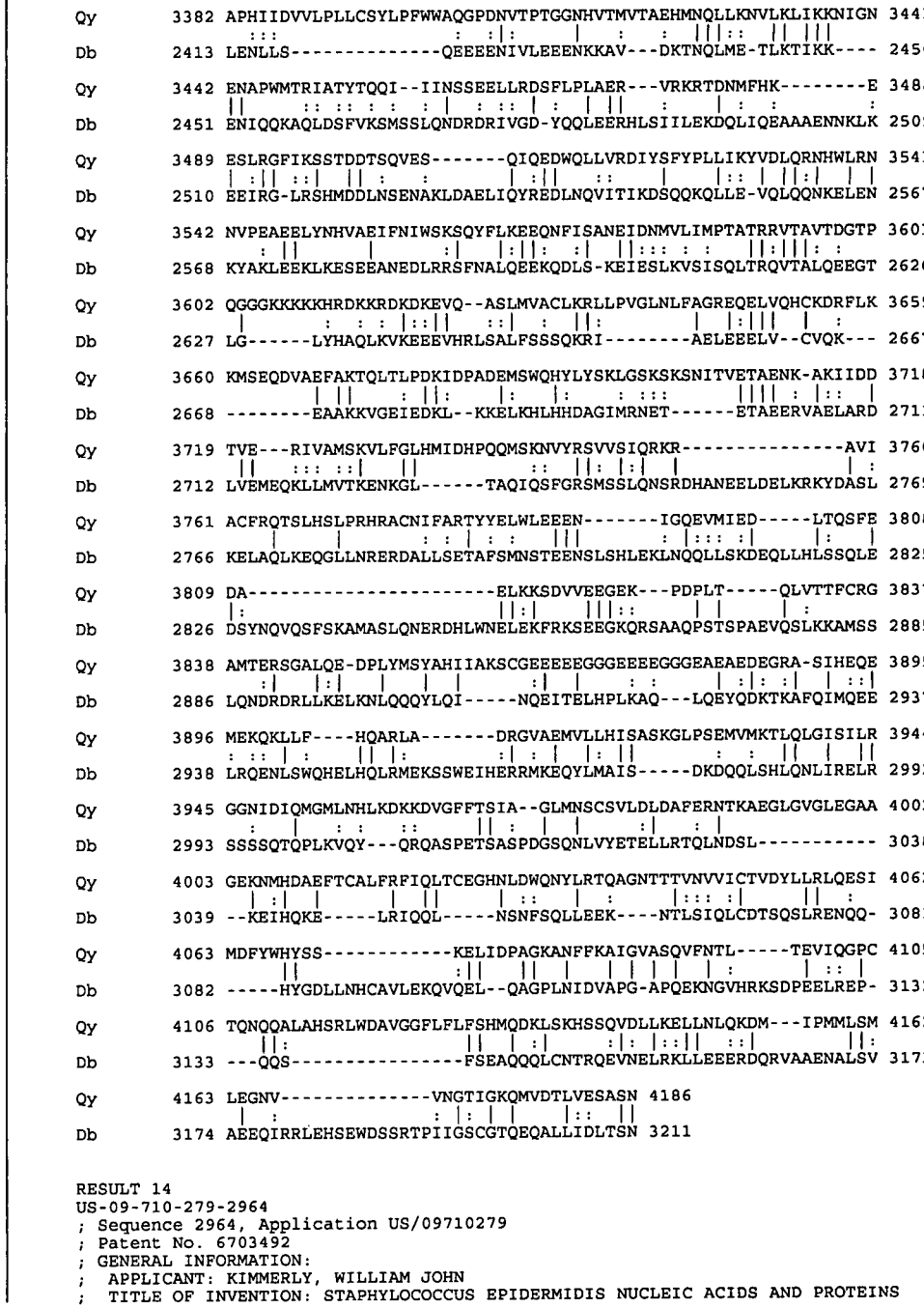
RESULT 8
US-08-114-555A-8
; Sequence 8, Application US/08114555A
; Patent No. 5854392
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
; TITLE OF INVENTION: RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

```
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,555A
;      FILING DATE:  30-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-114-555A-8

  Query Match             1.3%;  Score 336.5;  DB 1;  Length 240;
  Best Local Similarity   34.7%;  Pred. No. 2e-18;
  Matches   82;  Conservative   37;  Mismatches   70;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :          |  : |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW----------DPSFDK 1981
                 ||||||  |  |:|::|||  ||::|:  ||||:::| |  || :          :   ::
Db         65 DPVGGSVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEEEEEEEEE 124

Qy       1982 EGKDEHRK----------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 | :||  |                              ||| ||: |  ||||| ||::
Db        125 EEEDEEEKEEDEEEEEKEDAEKEEEEAPEGEKEDLEEGLLQMKLPESVKLQMCNLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||  : ::  : :|  |::|||| ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQ 240


RESULT 9
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF
;    TITLE OF INVENTION:  BETA APP-C100 RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036/2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,397A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869=8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-559-397A-14

  Query Match             1.3%;  Score 336.5;  DB 2;  Length 240;
  Best Local Similarity   34.7%;  Pred. No. 2e-18;
  Matches   82;  Conservative   37;  Mismatches   70;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :          |  : |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW----------DPSFDK 1981
                 ||||||  |  |:|::|||  ||::|:  ||||:::| |  || :          :   ::
Db         65 DPVGGSVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEEEEEEEEE 124

Qy       1982 EGKDEHRK----------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 | :||  |                              ||| ||: |  ||||| ||::
Db        125 EEEDEEEKEEDEEEEEKEDAEKEEEEAPEGEKEDLEEGLLQMKLPESVKLQMCNLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||  : ::  : :|  |::|||| ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQ 240


RESULT 10
US-08-114-555A-6
; Sequence 6, Application US/08114555A
; Patent No. 5854392
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF beta-APP-C100
;    TITLE OF INVENTION:  RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,555A
;      FILING DATE:  30-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-8864/9741
;      TELEX:  66141 PENNIE
```

```
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-114-555A-6

  Query Match             1.2%;  Score 334.5;  DB 1;  Length 240;
  Best Local Similarity   35.6%;  Pred. No. 3e-18;
  Matches   84;  Conservative   32;  Mismatches   73;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :         |     |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGK 1984
                 |||| | |  |:|::|||  ||::|:  ||||:::| |  || :       |   : | :
Db         65 DPVGASVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEDEEEEGEEE 124

Qy       1985 DEHRK--------------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 ||  |                               ||| ||: |  |||||:||::
Db        125 DEEEKEEDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||   ||   : :|  |::|||| ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQ 240


RESULT 11
US-08-559-397A-12
; Sequence 12, Application US/08559397A
; Patent No. 6083713
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF
;    TITLE OF INVENTION:  BETA APP-C100 RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036/2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,397A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869=8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-559-397A-12

  Query Match             1.2%;  Score 334.5;  DB 2;  Length 240;
  Best Local Similarity   35.6%;  Pred. No. 3e-18;
  Matches   84;  Conservative   32;  Mismatches   73;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :         |     |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGK 1984
                 |||| | |  |:|::|||  ||::|:  ||||:::| |  || :       |   : | :
Db         65 DPVGASVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEDEEEEGEEE 124

Qy       1985 DEHRK--------------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 ||  |                               ||| ||: |  |||||:||::
Db        125 DEEEKEEDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||   ||   : :|  |::|||| ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQ 240


RESULT 12
US-09-949-016-8849
; Sequence 8849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8849
;   LENGTH: 2262
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8849

  Query Match             1.2%;  Score 313.5;  DB 2;  Length 2262;
  Best Local Similarity   23.9%;  Pred. No. 1.2e-14;
  Matches  168;  Conservative  110;  Mismatches  263;  Indels  163;  Gaps   36;

Qy         76 LQELVTAAGSETGKGTGSGHRTLL-----YGNAILLRHLNSDMYLAC-LSTSSSQDKLAF 129
                |::|  ||  |  |    | :: ||      | | | | |: |: ||       :  : | |
Db         36 LKKLQHAAELEQ-KQNESENKKLLGEIVKYSNVIQLLHIKSNKYLTVNKRLPALLEKNAM 94

Qy        130 DVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK----EN--- 182
                | |   :  |  |: :||  | ||||: : ||| ::|: |   : || :      :|
Db         95 RVSLDA-AGNEGSWFYIHPFWKLRSEGDNIVVGDKVVLMPVNAGQPLHASNIELLDNPGC 153

Qy        183 -EVSIVNASFHVTHWSVQPYGTGISRMKYVGY----VFGGDVLRFFHGGDECLTIPSTWT 237
                 ||: || :   | | :  :       |||  |    : ||||:| ||   |       :
Db        154 KEVNAVNCN---TSWKITLF------MKYSSYREDVLKGGDVVRLFHAEQEKFLTCDEYE 204

Qy        238 KDGGQNI----VVYEGGSVMSQARSLWRLELA-RTKWAGGFINWYHPMRIRHITTGRYLG 292
                |   |:|     : :  :  : :::|| :|:       ||    |    | :|: || ||
Db        205 KK--QHIFLRTTLRQSATSATSSKALWEIEVVHHDPCRGGAGQWNSLFRFKHLATGNYLA 262

Qy        293 V-------NDQNE---------------------LY-LVS----------REEATTAS 311
                    : |||                      :| |||            :|||
Db        263 AELNPDYRDAQNEGKNVRDGVPPTSKKKRQAGEKIMYTLVSVPHGNDIASLFELDATTLQ 322

Qy        312 CAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSY----ETKK 367
                 | ||                          :| | ::|  |  |::  |     : ::
```

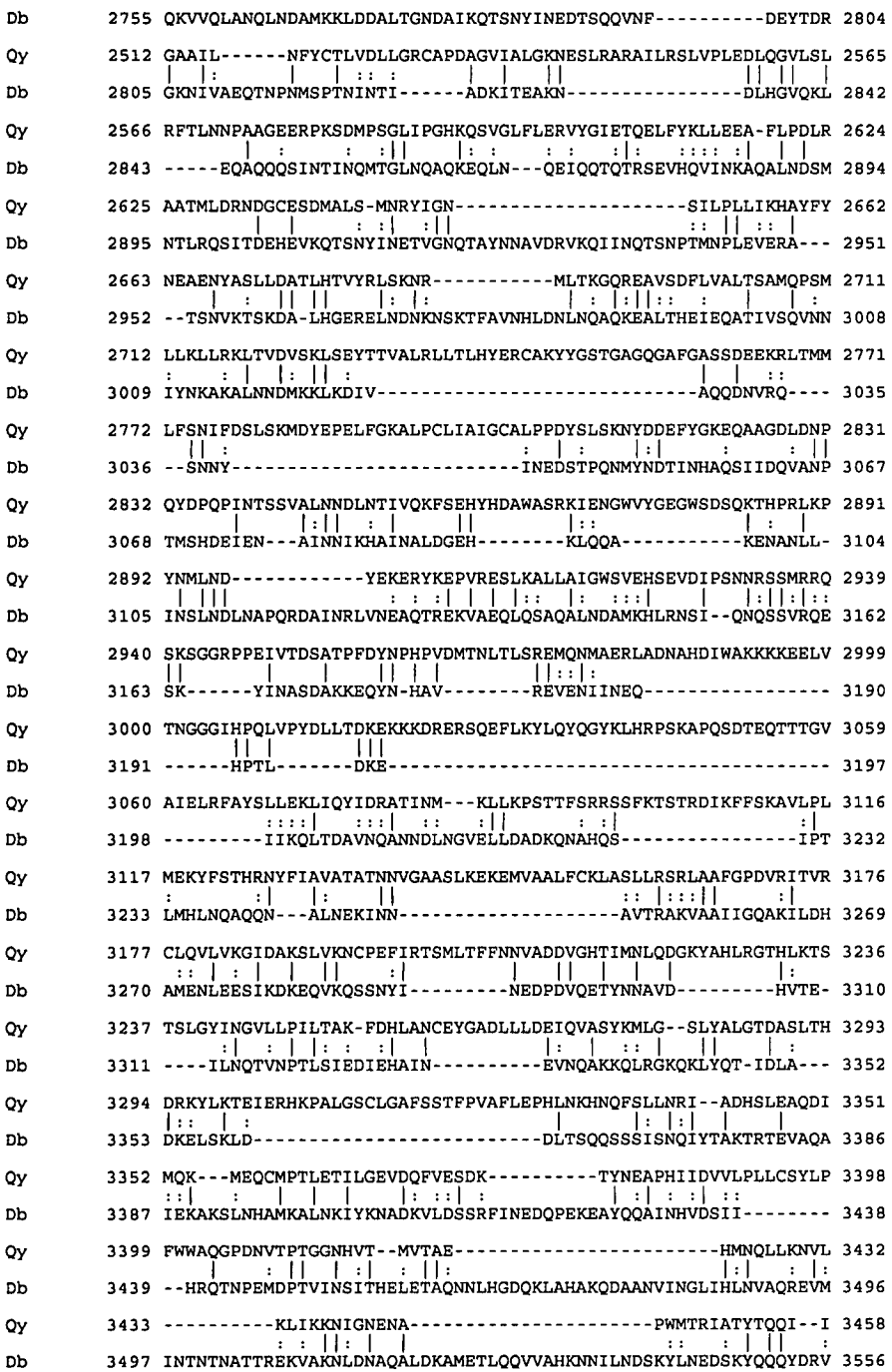
```
Db        323 RADCLVPR----------------------NSYVRLRHLCTNTWVTSTSIPIDTDEER 358

Qy        368 KGVGKV------EEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLE 421

Db        359 PVMLKIGTCQTKEDKEAFAIVSVPLSEVRDLDFANDANKVLATTVKKLE-------NG-- 409

Qy        422 TLQENRRHSMFFASVNLGEMVMCLEDLINYFAQ-PDEDMEHEE----KQNKFRALRNRQD 476

Db        410 TITQNERRF----------VTKLLEDLIFFVADVPNNGQEVLDVVITKPN-----RERQK 454

Qy        477 LFQEEGILNL---ILEAIDKINVITSQGFLAGFL-AGDESGQSWEMISGYLYQLLAAIIK 532

Db        455 LMREQNILAQVFGILKAPFKEK--AGEGSMLRLEDLGDQRYAPYKYMLRLCYRVL----- 507

Qy        533 GNHTNCAQFANSNRLNWLFSRLGSQASGEGTGML--DVLHCVLIDSPEALNM-MRDEHIK 589

Db        508 -RHSQQDYRKNQEYIAKNFCVMQSQI---GYDILAEDTITALLHNNRKLLEKHITAKEIE 563

Qy        590 VIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLL-PGK-NLLLQTALVDHVS 647

Db        564 TFVSLLRRN-REPRFLDYLSDLCVSNTTAIPVTQELICKFMLSPGNADILIQTKVVSMQA 622

Qy        648 S--VRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIG 689

Db        623 DNPMESSILSDDIDDEEVWLYWIDSNKEPHGKAIRHLAQEAKEG 666


RESULT 13
US-09-949-016-6507
; Sequence 6507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6507
;   LENGTH: 3259
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6507

  Query Match             1.1%;  Score 308;  DB 2;  Length 3259;
  Best Local Similarity   18.7%;  Pred. No. 6.8e-14;
  Matches  637;  Conservative  557;  Mismatches 1216;  Indels  988;  Gaps  171;

Qy       1283 NTFET--------MEKANWEFLRLSLPVICHN------EFIDEAEKA-RRWVEIKDRQQI 1327

Db        308 NTVETEREEESKILLEKMELEVAERKLSF--HNLQEEMHHLLEQFEQAGQAQAELESRYSA 365

Qy       1328 LMK--EAVEAQMPAHIDQIMRSG-------FTMNDIKGLHYEDNQEELPSS--KMKRLPS 1376

Db         366 LEQKHKAEMEEKTSHILSLQKTGQELQSACDALKDQNSKLLQDKNEQAVQSAQTIQQLED 425

Qy       1377 RPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAK-YDLGAQGLTPDDKKDKRGRS 1435

Db         426 QLQQKSK-----EISQFLNRLPLQ---QHETASQTSFPDVYNEGTQAVTEENIASLQKRV 477

Qy       1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495

Db         478 ----------------------------VELENEKGA---------------------- 486

Qy       1496 PSRTNLYGSQVGLNMATPTQDRKQMTTSTL--AQSATETVGNEIFDAECLKLINEYFYGV 1553

Db         487 -----LLLSSIELE-ELKAENEKLSSQITLLEAQNRTGEADREVSEISIVDIANKRSSSA 540

Qy       1554 RIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYM--- 1610

Db         541 E-ESGQD--------------VLENTFSQ-KHKELSVLLLE-----MKEAQEEIAFLKLQ 579

Qy       1611 ---VRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEP-ETK 1666

Db         580 LQGKRAEEADHEVLDQKEMK-QMEGEGI--------APIKMKVFLEDTGQDFPLMPNEES 630

Qy       1667 LFPAIFVEATSKEILQIELGRSATSLPLS---AAVLPTSDKH-------VIPQFP----- 1711

Db         631 SLPAVEKEQASTE------HQSRTSEEISLNDAGVELKSTKQDGDKSLSAVPDIGQCHQD 684

Qy       1712 --PRLKVQCLKP----HQWARVPNQSLQVHALK-------------------------- 1738

Db         685 ELERLKSQILELELNFHKAQEIYEKNLDEKAKEISNLNQLIEEFKKNADNNSSAFTALSE 744

Qy       1739 -----LSDIRGWSMLCE--DAVSMLALHIPEED--RCIDILEPIEMDKLLSFHSHTLTLY 1789

Db         745 ERDQLLSQVKELSMVTELRAQVKQLEMNLAEAERQRRLDYESQTAHDNLLTEQIHSLSIE 804

Qy       1790 AALCYQSNYRAAHALCTHVDQKQLLYAIQS---QYMSGPLRQGFYDLLIAL----HLESH 1842

Db         805 A----KSKDVKIEVLQNELDDVQLQFSEQSTLIRSLQSQLQNKESEVLEGAERVRHISSK 860

Qy       1843 ATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITE-ISNL 1901

Db         861 VEELSQALSQKELEITKMDQLLLEKK---RDVETLQQTIEEKDQQVTEISFSMTEKMVQL 917

Qy       1902 YSPYFPLEVAREFVMQAL-----AEAVETNQVHNRDPV-GGSNENLFLPLIKLVDRLLLV 1955

Db         918 NEEKFSLGVEIKTLKEQLNLLSRAEEAKKEQVEEDNEVSSGLKQN--------YDEMSPA 969

Qy       1956 GMMRDEDVEKLLIMTNPETWDPSFD---KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLN 2012

Db         970 GQISKEELQH------------EFDLLKKENEQRKRK-------LQAALINRKELLQRVS 1010

Qy       2013 DIQ-----LRHRVEAIIAFAHDFVGDLQTD-QLRRYTEIKQSDLPSAVAAKKTREFRCPP 2066

Db        1011 RLEEELANLKDESKKEIPLSETERGEVEEDKENKEYSE--------KCVTSKCQEIEIYL 1062

Qy       2067 REQMN-AILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQ--- 2122

Db        1063 KQTISEKEVELQHIRKDLEEKLAAEEQFQALVKQMNQTLQDKTNQIDLLQAEISENQAII 1122

Qy       2123 ------EPEAKPG---AFGKLYNIINT---------VKELEEEAKAIEEPPKKTPEEKFR 2164

Db        1123 QKLITSNTDASDGDSVALVKETVVISPPCTGSSEHWKPELEEKILALEK-EKEQLQKKLQ 1181

Qy       2165 KVLI--QTIVNWAEESQ---IETPKLVREMFSLLVRQYDA-------VGELIRALEKTYV 2212

Db        1182 EALTSRKAILKKAQEKERHLREELKQQKDDYNRLQEQFDEQSKENENIGDQLRQLQ---- 1237

Qy       2213 INAKTKLDVAEMWVGLSQIRALLPVQMSQEEEEL------MRKRLWKLVNNHTFFQHPDL 2266

Db        1238 IQVRESID------------GKLP---STDQQESCSSTPGLEEPLFKATEQH----HTQP 1278

Qy       2267 IRVLRV-------HENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACC 2319

Db        1279 VLESNLCPDWPSHSEDASALQGGTSVAQIKAQL-KEIEAEKVELELKVSSTTSELT---- 1333

Qy       2320 RFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRG-STPLDVAYSSL---MENTEL 2375

Db        1334 --------------KKSEEVFQLQEQINKQGLEIESLKTVSHEAEVHAESLQQKLESSQL 1379

Qy       2376 ALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESV 2435

Db        1380 QIAGLEHLRE------LQPKLDELQKLISKKEEDVS----------------YLSGQLS 1416

Qy       2436 EENANLV-IRLLIRRPECLGPALRGEGEGLLKAI-----VDANKMSERIADRR-KLREME 2488
```

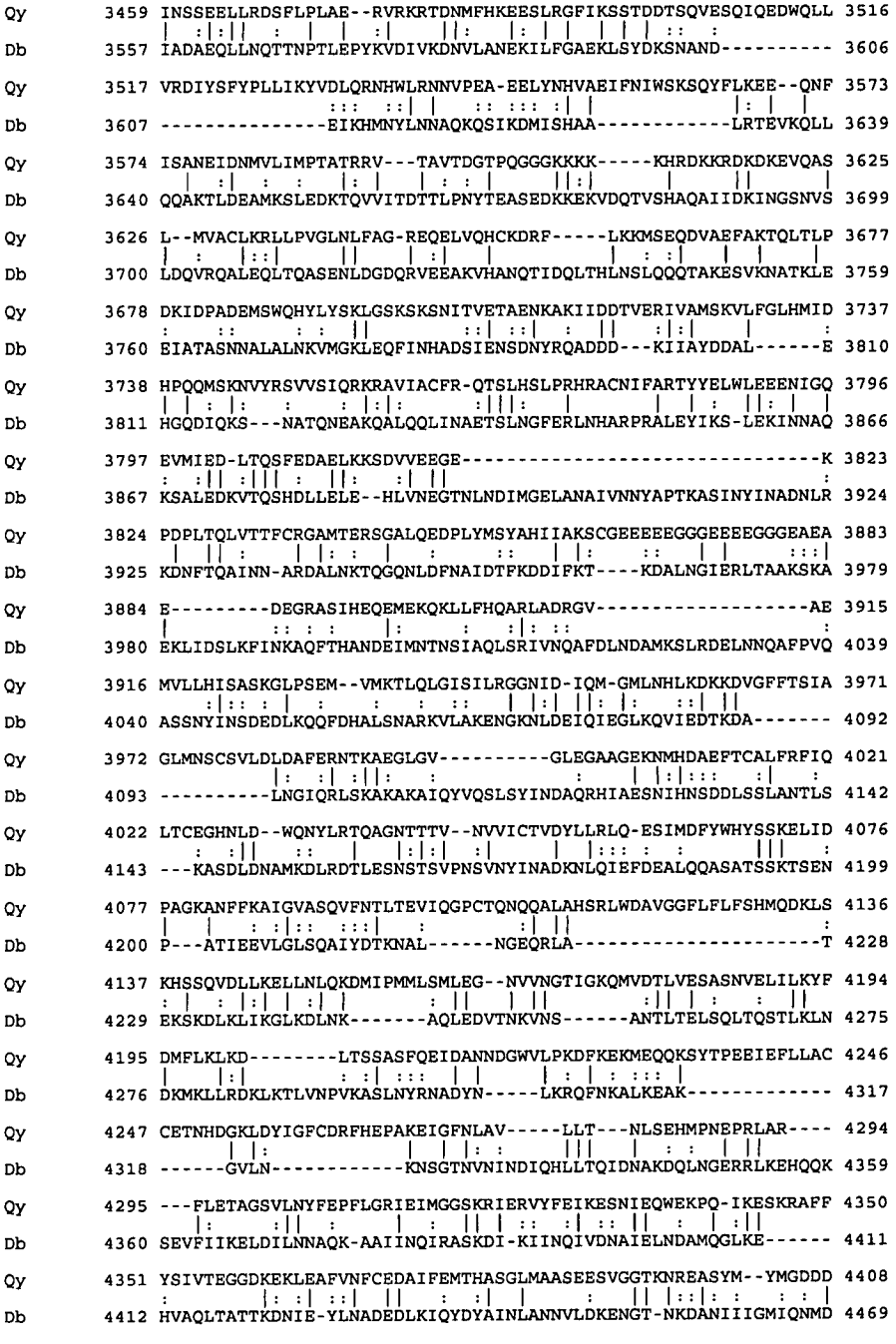




RESULT 14
US-09-710-279-2964
; Sequence 2964, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

```
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
;  LENGTH: 5024
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: synthetic
;  OTHER INFORMATION: amino acid sequence
;  FEATURE:
;  NAME/KEY: MOD_RES
;  LOCATION: (5024)
;  OTHER INFORMATION: variable amino acid
US-09-710-279-2964

  Query Match             1.1%;  Score 305.5;  DB 2;  Length 5024;
  Best Local Similarity   17.1%;  Pred. No. 2.5e-13;
  Matches  788;  Conservative  674;  Mismatches 1619;  Indels 1523;  Gaps  206;

Qy       839 SKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYG 898
Db      1323 AEQALHGAEKLNQDKQTSSTELD----GLTDLTDAQREKLREQINT----------S 1365

Qy       899 DQREDL-HKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRL 957
Db      1366 NSRDDIKQKIEQA----KALNDAMKKLKEQVAQK--DGVHANSDYTNEDSAQKDAYNNAL 1419

Qy       958 PNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSD 1017
Db      1420 KQAEDIINNSSNP---NLNAQDITNALNN-IKQAQDNLH---GAQKLQQ----DKNTTNQ 1468

Qy      1018 MHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQA 1077
Db      1469 AIGNLNHLNQPQKDALIQAINGATSRDQVAEKLKEAEALD----------EAMKQLE- 1515

Qy      1078 DFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEE 1137
Db      1516 ----------------------------------------------------DQVNQD 1521

Qy      1138 KVYSGNT----ESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGD 1193
Db      1522 DQISNSSPFINEDSDKQKTYNDKIQAAKEIINQTSNPTLDKQKIADTL----------Q 1570

Qy      1194 NFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVT-----HWYTKD 1248
Db      1571 NIKDAVNNLHGDQKLAQSKQDANNQ---------------LNHLDDLTEEQKNHF---- 1610

Qy      1249 QPIFENTD--EMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHN 1306
Db      1611 KPLINNADTRDEVNKQLEIAK-QLNGDMSTLHKVINDKDQIQHLSNY--------INADN 1661

Qy      1307 EFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGF--TMNDIKGLHYEDNQE 1364
Db      1662 DKKQNYDNA-----IKEAEDLIHN---------HPDTLDHKALQDLLNKIDQAHNELNGE 1707

Qy      1365 ------------ELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412
Db      1708 SRFKQALDNALNDIDSLNSLNVPQRQTVKDNINHVTTLESL----------AQELQ 1753

Qy      1413 MAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERG 1472
Db      1754 KAK----------ELNDA--------MKAMRDSIMNQEQIRKNSN---YTNEDLAQQNA 1791

Qy      1473 ARRP----------NPQIKVSQA----NQRYNGMNA----RPSRTNLYGSQVGLN 1509
Db      1792 YNHAVDNINNIIGEDNATMDPQI-IKQATQDINTAINGLNGDQKLQDAKTD--AKQQITN 1848

Qy      1510 MATPTQDRKQMTTSTL-AQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGW 1568

Db      1849 FTGLTEPQKQALENIINQQTSRANVAKQLSHA---KFLNGKMEELKV---------- 1892

Qy      1569 VTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKG 1628
Db      1893 --------------AVAKASLV----------RQNSNYINEDVSEKEAYEQAIAKG 1924

Qy      1629 ASQGMFIGCSVDTSTGSVSFTCEGKD-TSFKFKMEPETKLFPAIFVEATSKEILQIELGR 1687
Db      1925 QE---IINSENNPTISSTDINRTIQEINDAEQNLHGENKLRQA--QEIAKNEIQNLDGLN 1979

Qy      1688 SATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLSD----IR 1743
Db      1980 SAQITKLIQDIGRTTTKPAVTQ----------KLEEAKAINQAMQQLKQSIADKDATLN 2028

Qy      1744 GWSMLCEDAVSMLALH--IPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAA 1801
Db      2029 SSNYLNEDSEKKLAYDNAVSQAEQLINQLNDPTMD-ISNIQAITQKVIQA---KDSLHGA 2084

Qy      1802 HALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTME------ACKNEFVI 1855
Db      2085 NKLAQNQADSNLIIN-QSTNLNDKQKQALNDLI------NHAQTKQQVAEIIAQANKLNN 2137

Qy      1856 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1915
Db      2138 EMG-TLKTLVEEQSNVHQQSKYINED--PQ----------VQNIYND--SIQKGREIL 2180

Qy      1916 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN---- 1971
Db      2181 NGT------TDDVLNNNKIADAIQNIHLTKNDLHGDQKLQKAQQDA-TNELNYLTNLNNS 2233

Qy      1972 --PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHD 2029
Db      2234 QRQSEHDEINSAPSRTEVSNDLNHAKALNEAMRQL------ENEVALENSVKKL----SD 2283

Qy      2030 FVGDLQTDQLRRYTEIKQ------SDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEED 2083
Db      2284 FINEDEAAQ-NEYSNALQKAKDIINGVPSSTLDKATIE---------DALLELQNARE-- 2331

Qy      2084 KENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-------PEAKPG---AFGK 2133
Db      2332 ------------------------SLHGEQKLQEAKNQAIAEIDNLQALNPGQVLAEKT 2366

Qy      2134 LYNIINTVKELEE---EAKAIEEPPKKTPEEKFRKVLIQ----------------TIVN 2173
Db      2367 LVNQASTKPEVQEALQKAKELNEAMKALKTEINKKEQIKADSRYVNADSGLQANYNSALN 2426

Qy      2174 WAEE--SQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVA--------E 2223
Db      2427 YGSQIIATTQPPELNKDVI-------NRATQTIKTAENN--LNGQSKLAEAKSDGNQSIE 2477

Qy      2224 MWVGLSQIR------ALLPVQMSQEEEELMR---------KRLWKLVNN-HTFFQHPDLI 2267
Db      2478 HLQGLTQSQKDKQHDLINQAQTKQQVDDIVNNSKQLDNSMNQLQQIVNNDNTVKQNSDFI 2537

Qy      2268 R----------------VLRVHENVM--AVMMNTLGRRAQAQSDAQPSSQPVAEDSKE 2307
Db      2538 NEDSSQQDAYNHAIQAAKDLITAHPTIMDKNQIDQAIENIKQALNDLHGSNK-LSEDKKE 2596

Qy      2308 --------------KDT--SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNIL 2350
Db      2597 ASEQLQNLNSLTNGQKDTILNHIFSAPTRSQVGEKIASAKQLNNTMKALRDSIADNNEIL 2656

Qy      2351 LSRPSLRGSTPLDVAYSS--------------LMENTELALALREHYLEKIAVYLSRCG 2395
Db      2657 QSSKYFNEDSEQQNAYNQAVNKAKNIINDQPTPVMANDEIQSVLNE-------VKQTKDN 2709

Qy      2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWV---NGESVEENANLVIRLLIRRPEC 2452
Db      2710 LHGDQKLAN--------DKTDAQATLNALNYLNQAQRGNLETKVQNSN-------SRPEV 2754

Qy      2453 LGPA-LRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
```



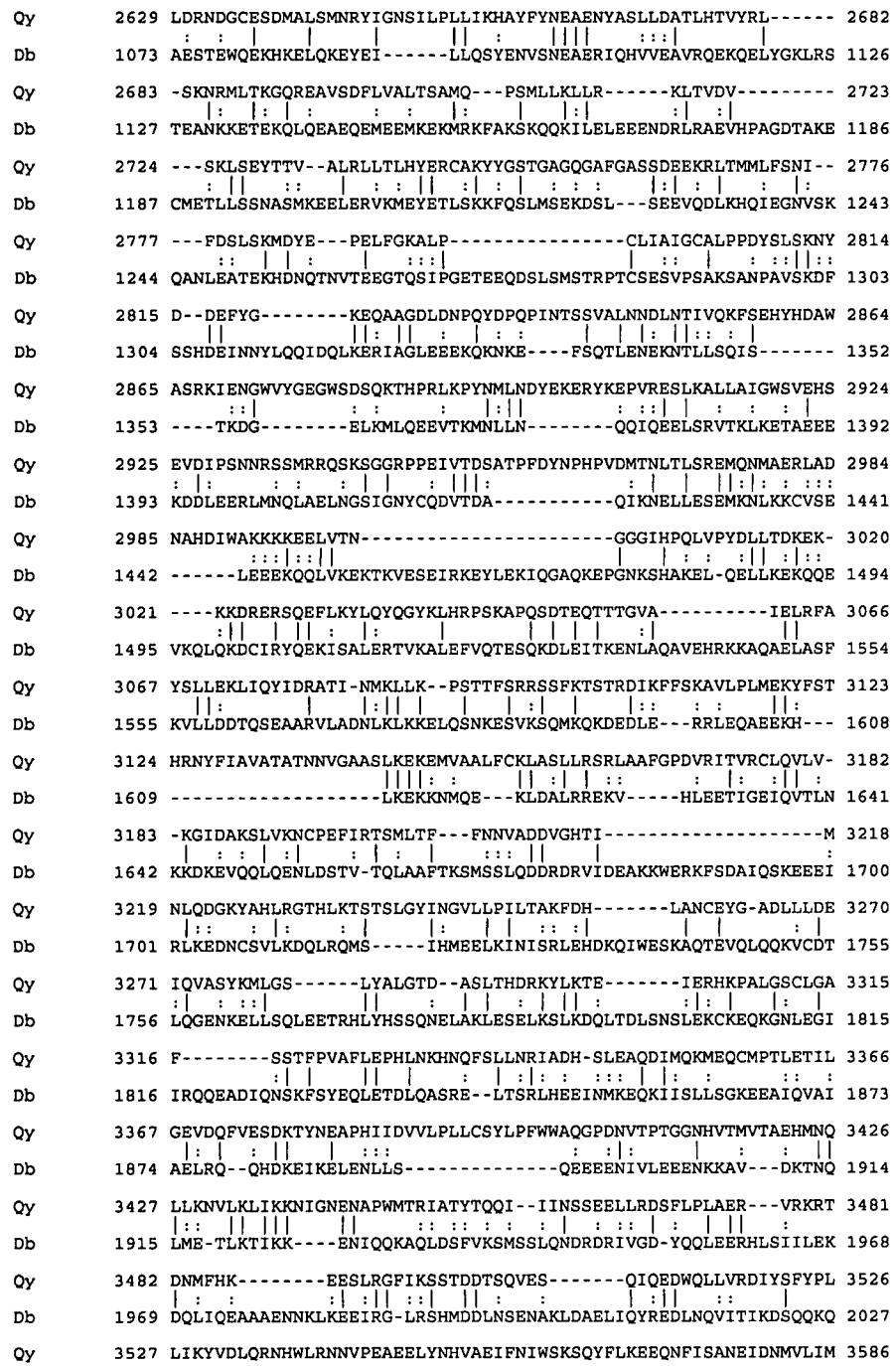


```
Qy       4409 DERAGKDPFRRGLQSVKDGVATAFSSL--------------SPSNIKAKIADMQQMPPA 4453
Db       4470 DARA----LLNGIERLKDAQTKAHNDIKDTLKRQLDEIEHANATSNSKAQ---AKQMVNE 4522

Qy       4454 ELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHR 4513
Db       4523 EARKAFSNI-----------------------------------NHATSNDLVNQAKDE 4546

Qy       4514 LLATQSSRHLPALPPAD-DTGQMQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAE 4572
Db       4547 GQSAIEHIHADELPKAKLDANQM------IDQKVEDINHL-------------------- 4580

Qy       4573 VSPDESADHTEEQRPPSLID-LLGGEQAKKQAQERMEAQAAQQAA--MSAIEAESKKAVQ 4629
Db       4581 ISQNPNLSNEEKNKLISQINKLVNG--IKNEIQQAINKQQIENATTKLDEVIETTKKLII 4638

Qy       4630 GPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEG 4689
Db       4639 AKAEAKQVIKELSQKKRDAINNNTDLTPSQKAHALA-----------------DIDKTEK 4681

Qy       4690 SGLGDIIAGGGSGSGAGSGSGDGSGESGE------------DDDALEVVHIDEDFFYMEH 4737
Db       4682 DALQHI---------ENSNSIDDINNNKEHAFNTLAHIIIWDTDQQPLVFELPELSLQNA 4732

Qy       4738 VIKMAAVLH--SIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKS 4795
Db       4733 LVTSEVVVHRDETISLESIIGAMTLTDELKV---------------NIVSLPNTDKVAD 4776

Qy       4796 HWD---KLVISAKSF-----PVNYWDK---------------FVKKKVRAKYSETYDFDS 4832
Db       4777 HLTAKVKVILADGSFVTVNVPVKVVEKELQIAKKDAIKTIDVLVKQKIK-------DIDS 4829

Qy       4833 ISNMLGMEKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVM 4892
Db       4830 NNELTSTQREDAKAEIERLKKQAIDKVTH----------SKSIKD---IETVKRTDFEEI 4876

Qy       4893 GNFNNFFFAAH------LLDVAV----GFKTLRTILQSVTHNGK 4926
Db       4877 DQFDPKRFTLNKAKKDIITDVNTQIQNGFKEIETI-KGLTSNEK 4919
```

RESULT 15
US-09-949-016-11433
; Sequence 11433, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11433
; LENGTH: 2733
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11433

Query Match 1.1%; Score 305; DB 2; Length 2733;
Best Local Similarity 19.0%; Pred. No. 8.5e-14;
Matches 570; Conservative 497; Mismatches 1070; Indels 856; Gaps 150;

```
Qy       1653 KDTSFKFKMEP-ETKLFPAIFVEATSKEILQIELGRSATSLPLS---AAVLPTSDKH--- 1705
Db         90 EDTGQDFPLMPNEESSLPAVEKEQASTE------HQSRTSEEISLNDAGVELKSTKQDGD 143

Qy       1706 ----VIPQFP-------PRLKVQCLKP----HQWARVPNQSLQVHALK----------- 1738
Db        144 KSLSAVPDIGQCHQDELERLKSQILELELNFHKAQEIYEKNLDEKAKEISNLNQLIEEFK 203

Qy       1739 -------------------LSDIRGWSMLCE--DAVSMLALHIPEED--RCIDILEPIE 1774
Db        204 KNADNNSSAFTALSEERDQLLSQVKELSMVTELRAQVKQLEMNLAEAERQRRLDYESQTA 263

Qy       1775 MDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQS---QYMSGPLRQGFY 1831
Db        264 HDNLLTEQIHSLSIEA----KSKDVKIEVLQNELDDVQLQFSEQSTLIRSLQSQLQNKES 319

Qy       1832 DLLIAL----HLESHATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMK 1887
Db        320 EVLEGAERVRHISSKVEELSQALSQKELEITKMDQLLLEKK---RDVETLQQTIEEKDQQ 376

Qy       1888 MTDIAESITE-ISNLYSPYFPLEVAREFVMQAL-----AEAVETNQVHNRDPV-GGSNEN 1940
Db        377 VTEISFSMTEKMVQLNEEKFSLGVEIKTLKEQLNLLSRAEEAKKEQVEEDNEVSSGLKQN 436

Qy       1941 LFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD---KEGKDEHRKGLLHMKMA 1997
Db        437 --------YDEMSPAGQISKEELQH------------EFDLLKKENEQRKRK-------L 469

Qy       1998 EGAKLQMCYLLQHLNDIQ-----LRHRVEAIIAFAHDFVGDLQTD-QLRRYTEIKQSDLP 2051
Db        470 QAALINRKELLQRVSRLEEELANLKDESKKEIPLSETERGEVEEDKENKEYSE------- 522

Qy       2052 SAVAAKKTREFRCPPREQMN-AILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSL 2110
Db        523 -KCVTSKCQEIEIYLKQTISEKEVELQHIRKDLEEKLAAEEQFQALVKQMNQTLQDKTNQ 581

Qy       2111 HALQEPDAAENQ---------EPEAKPG---AFGKLYNIINT---------VKELEEEAK 2149
Db        582 IDLLQAEISENQAIIQKLITSNTDASDGDSVALVKETVVISPPCTGSSEHWKPELEEKIL 641

Qy       2150 AIEEPPKKTPEEKFRKVLI--QTIVNWAEESQ---IETPKLVREMFSLLVRQYDA----- 2199
Db        642 ALEK-EKEQLQKKLQEALTSRKAILKKAQEKERHLREELKQQKDDYNRLQEQFDEQSKEN 700

Qy       2200 --VGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEEL------MRKRL 2251
Db        701 ENIGDQLRQLQ----IQVRESID-----------GKLP---STDQQESCSSTPGLEEPL 741

Qy       2252 WKLVNNHTFFQHPDLIRVLRV-------HENVMAVMMNTLGRRAQAQSDAQPSSQPVAED 2304
Db        742 FKATEQH----HTQPVLESNLCPDWPSHSEDASALQGGTSVAQIKAQL-KEIEAEKVELE 796

Qy       2305 SKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRG-STPLD 2363
Db        797 LKVSSTTSELT-----------------KKSEEVFQLQEQINKQGLEIESLKTVSHEAE 838

Qy       2364 VAYSSL---MENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERY 2420
Db        839 VHAESLQQKLESSQLQIAGLEHLRE------LQPKLDELQKLISKKEEDVS--------- 883

Qy       2421 LDFLRFCVWVNGESVEENANLV-IRLLIRRPECLGPALRGEGEGLLKAI-----VDANKM 2474
Db        884 --------YLSGQLSEKEAALTKIQTEII----------EQEDLIKALHTQLEMQAKEH 924

Qy       2475 SERIADRR-KLREMEQEGDVNFSHPLPESDEDEDYI------DTGAAILNFYCTLVDLLG 2527
Db        925 DERIKQLQVELCEMKQK---------PEEIGEESRAKQQIQRKLQAALI---------- 964

Qy       2528 RCAPDAGVIALGKNESLR-----ARAILRSLV-PLEDLQGVLSLRFTLNNPAAG------ 2575
Db        965 -----SRKEALKENKSLQEELSLARGTIERLTKSLADVESQVSAQNKEKDTVLGRLALLQ 1019

Qy       2576 EERPK--SDMPSGLIPGHK-----QSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATM 2628
Db       1020 EERDKLITEMDRSLLENQSLSSSCESLKLALEGL--TEDKE---KLVKE--IESLKSSKI 1072
```



Search completed: October 6, 2006, 23:35:39
Job time : 144 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 6, 2006, 23:58:04 ; Search time 465 Seconds
(without alignments)
5108.314 Million cell updates/sec

Title: US-10-668-767-128
Perfect score: 26800
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....WDFFPVGDCFRKQYEDLMGE 5128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26800	100.0	5128	4	US-10-668-767-128	Sequence 128, App
2	26716	99.7	5134	4	US-10-668-767-130	Sequence 130, App
3	26644	99.4	5142	4	US-10-668-767-144	Sequence 144, App
4	26506	98.9	5100	4	US-10-668-767-146	Sequence 146, App
5	26469	98.8	5142	4	US-10-668-767-2	Sequence 2, Appli
6	21630	80.7	5127	4	US-10-668-767-8	Sequence 8, Appli
7	21403	79.9	5127	4	US-10-668-767-122	Sequence 122, App
8	21376	79.8	5113	4	US-10-668-767-121	Sequence 121, App
9	21360	79.7	5127	4	US-10-668-767-120	Sequence 120, App
10	21326	79.6	5109	4	US-10-668-767-10	Sequence 10, Appl
11	21270.5	79.4	5107	6	US-11-097-143-22563	Sequence 22563, A
12	21234.5	79.2	5112	4	US-10-668-767-125	Sequence 125, App
13	21218.5	79.2	5126	4	US-10-668-767-56	Sequence 56, Appl
14	21218.5	79.2	5126	4	US-10-668-767-124	Sequence 124, App
15	21191.5	79.1	5112	4	US-10-668-767-126	Sequence 126, App
16	21175.5	79.0	5126	4	US-10-668-767-123	Sequence 123, App
17	21046	78.5	5104	4	US-10-668-767-6	Sequence 6, Appli
18	20932.5	78.1	5101	4	US-10-668-767-4	Sequence 4, Appli
19	20422.5	76.2	4868	4	US-10-668-767-57	Sequence 57, Appl
20	12129	45.3	5317	4	US-10-668-767-59	Sequence 59, Appl
21	11938.5	44.5	5071	4	US-10-668-767-58	Sequence 58, Appl
22	11887.5	44.4	4968	4	US-10-668-767-61	Sequence 61, Appl
23	11868	44.3	4967	4	US-10-668-767-62	Sequence 62, Appl
24	11840	44.2	4967	4	US-10-668-767-60	Sequence 60, Appl
25	11561	43.1	5107	4	US-10-369-493-6377	Sequence 6377, Ap
26	11453.5	42.7	4868	6	US-11-044-111-24	Sequence 24, Appl
27	11407.5	42.6	4870	4	US-10-764-425-144	Sequence 144, App
28	11347.5	42.3	5038	5	US-10-723-860-1310	Sequence 1310, Ap
29	11347.5	42.3	5038	5	US-10-756-149-5039	Sequence 5039, Ap
30	11347.5	42.3	5081	5	US-10-450-763-35328	Sequence 35328, A
31	11338.5	42.3	5081	4	US-10-276-774-1850	Sequence 1850, Ap
32	11325.5	42.3	5032	4	US-10-408-765A-26	Sequence 26, Appl
33	11325	42.3	4899	5	US-10-450-763-42673	Sequence 42673, A
34	11222	41.9	4934	5	US-10-450-763-53705	Sequence 53705, A
35	10863.5	40.5	4767	4	US-10-276-774-1902	Sequence 1902, Ap
36	8109	30.3	3647	4	US-10-408-765A-2436	Sequence 2436, Ap
37	7530.5	28.1	3375	6	US-11-044-111-23	Sequence 23, Appl
38	4953	18.5	2055	4	US-10-276-774-1795	Sequence 1795, Ap
39	2709.5	10.1	1056	6	US-11-044-111-22	Sequence 22, Appl
40	1146.5	4.3	1425	5	US-10-450-763-53703	Sequence 53703, A
41	847	3.2	249	5	US-10-784-004-338	Sequence 338, App
42	730.5	2.7	323	5	US-10-450-763-35329	Sequence 35329, A
43	723.5	2.7	616	5	US-10-450-763-53704	Sequence 53704, A
44	712	2.7	1232	5	US-10-450-763-34060	Sequence 34060, A
45	698.5	2.6	599	5	US-10-450-763-53702	Sequence 53702, A

ALIGNMENTS

RESULT 1
US-10-668-767-128
; Sequence 128, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 5128
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv7
US-10-668-767-128

Query Match 100.0%; Score 26800; DB 4; Length 5128;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
```

```
Qy      241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Qy      301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Qy      361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Qy      421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Qy      481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Qy      541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Qy      601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Qy      661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Qy      721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780

Qy      781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Qy      841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Qy      901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Qy      961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020

Qy     1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

Qy     1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140

Qy     1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200

Qy     1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260

Qy     1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320

Qy     1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380

Qy     1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440

Qy     1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500

Qy     1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560

Qy     1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620

Qy     1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680

Qy     1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740

Qy     1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800

Qy     1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860

Qy     1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920

Qy     1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980

Qy     1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Qy     2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100

Qy     2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160

Qy     2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy     2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy     2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340

Qy     2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy     2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880

Qy       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000

Qy       3001 NGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGVA 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 NGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGVA 3060

Qy       3061 IELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLMEKY 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 IELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLMEKY 3120

Qy       3121 FSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQV 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 FSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQV 3180

Qy       3181 LVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 LVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLG 3240

Qy       3241 YINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 YINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKT 3300

Qy       3301 EIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCMP 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 EIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCMP 3360

Qy       3361 TLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTMVT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTMVT 3420

Qy       3421 AEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRKR 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRKR 3480

Qy       3481 TDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWLR 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWLR 3540

Qy       3541 NNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDGT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 NNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDGT 3600

Qy       3601 PQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLKK 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 PQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLKK 3660

Qy       3661 MSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKIIDDTV 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 MSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKIIDDTV 3720

Qy       3721 ERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIF 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 ERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIF 3780

Qy       3781 ARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMT 3840

Qy       3841 ERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQK 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 ERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQK 3900

Qy       3901 LLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKD 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 LLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKD 3960

Qy       3961 KKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFI 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 KKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFI 4020

Qy       4021 QLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGK 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 QLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGK 4080

Qy       4081 ANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSS 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 ANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSS 4140

Qy       4141 QVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKL 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 QVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKL 4200

Qy       4201 KDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGF 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 KDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGF 4260

Qy       4261 CDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSK 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSK 4320

Qy       4321 RIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 RIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHA 4380

Qy       4381 SGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNI 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 SGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNI 4440

Qy       4441 KAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPE 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 KAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPE 4500

Qy       4501 PTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESP 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 PTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESP 4560

Qy       4561 STSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAI 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 STSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAI 4620
```

```
Qy       4621 EAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVS 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 EAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVS 4680

Qy       4681 TLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYMEHVIK 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYMEHVIK 4740

Qy       4741 MAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKL 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 MAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKL 4800

Qy       4801 VISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYII 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 VISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYII 4860

Qy       4861 NIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQS 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 NIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQS 4920

Qy       4921 VTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 VTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKG 4980

Qy       4981 VRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESV 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 VRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESV 5040

Qy       5041 KEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYV 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 KEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYV 5100

Qy       5101 WNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128
             |||||||||||||||||||||||||||||
Db       5101 WNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128
```

RESULT 2
US-10-668-767-130
; Sequence 130, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 5134
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv2
US-10-668-767-130

Query Match 99.7%; Score 26716; DB 4; Length 5134;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 5117; Conservative 4; Mismatches 7; Indels 6; Gaps 2;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKPAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KSYETKKEGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        661 SAVYRKWYFEVTMDHIEKTTHMIPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
```

```
Qy      1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
Db      1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200

Qy      1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
Db      1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260

Qy      1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
Db      1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320

Qy      1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380
Db      1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380

Qy      1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440
Db      1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440

Qy      1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500
Db      1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500

Qy      1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560
Db      1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560

Qy      1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620
Db      1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620

Qy      1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680
Db      1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680

Qy      1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740
Db      1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740

Qy      1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
Db      1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800

Qy      1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
Db      1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860

Qy      1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920
Db      1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFVMQALA 1920

Qy      1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
Db      1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980

Qy      1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
Db      1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Qy      2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100
Db      2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100

Qy      2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
Db      2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160

Qy      2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
Db      2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy      2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
Db      2221 VAGMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy      2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340
Db      2281 MNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340

Qy      2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
Db      2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy      2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
Db      2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy      2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
Db      2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy      2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
Db      2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy      2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
Db      2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy      2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
Db      2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy      2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
Db      2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy      2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
Db      2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy      2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880
Db      2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880

Qy      2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
Db      2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy      2941 KSGGRPPEIV-TDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 2999
Db      2941 KSGGRPPEIVQTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 3000

Qy      3000 TNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGV 3059
Db      3001 TNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGV 3060

Qy      3060 AIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLMEK 3119
Db      3061 AIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKVVLPLMEK 3120

Qy      3120 YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQ 3179
Db      3121 YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQ 3180

Qy      3180 VLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSL 3239
Db      3181 VLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSL 3240

Qy      3240 GYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLK 3299
Db      3241 GYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLK 3300

Qy      3300 TEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCM 3359
```

```
Db       3301 TEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCM 3360
Qy       3360 PTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTMV 3419
Db       3361 PTLEAILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTMV 3420
Qy       3420 TAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRK 3479
Db       3421 TAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRK 3480
Qy       3480 RTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWL 3539
Db       3481 RTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWL 3540
Qy       3540 RNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDG 3599
Db       3541 RNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDG 3600
Qy       3600 TPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRF-- 3657
Db       3601 TPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLK 3660
Qy       3658 ---LKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAK 3714
Db       3661 VGTLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAK 3720
Qy       3715 IIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRH 3774
Db       3721 IIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRH 3780
Qy       3775 RACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTF 3834
Db       3781 RACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTF 3840
Qy       3835 CRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQ 3894
Db       3841 CRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQ 3900
Qy       3895 EMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGM 3954
Db       3901 EMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGM 3960
Qy       3955 LNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTC 4014
Db       3961 LNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTC 4020
Qy       4015 ALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKEL 4074
Db       4021 ALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKEL 4080
Qy       4075 IDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDK 4134
Db       4081 IDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDK 4140
Qy       4135 LSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYF 4194
Db       4141 LSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYF 4200
Qy       4195 DMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGK 4254
Db       4201 DMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGK 4260
Qy       4255 LDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4314
Db       4261 LDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4320
Qy       4315 IMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAI 4374
Db       4321 IMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAI 4380
Qy       4375 FEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSS 4434
Db       4381 FEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSS 4440
Qy       4435 LSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQT 4494
Db       4441 LSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQT 4500
Qy       4495 DEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQV 4554
Db       4501 DEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQV 4560
Qy       4555 KPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQ 4614
Db       4561 KPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQ 4620
Qy       4615 AAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVL 4674
Db       4621 AAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVL 4680
Qy       4675 LFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFY 4734
Db       4681 LFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFY 4740
Qy       4735 MEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLK 4794
Db       4741 MEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLK 4800
Qy       4795 SHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKG 4854
Db       4801 SHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKG 4860
Qy       4855 LIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTL 4914
Db       4861 LIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTL 4920
Qy       4915 RTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFV 4974
Db       4921 RTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFV 4980
Qy       4975 FNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELR 5034
Db       4981 FNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELR 5040
Qy       5035 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYT 5094
Db       5041 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYT 5100
Qy       5095 GQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128
Db       5101 GQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5134
```

RESULT 3
US-10-668-767-144
; Sequence 144, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 144
; LENGTH: 5142
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv3
US-10-668-767-144

Query Match 99.4%; Score 26644; DB 4; Length 5142;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 5107; Conservative 6; Mismatches 15; Indels 14; Gaps 3;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||     |||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEATTASCAFCLRQEKGDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 DLFQEEGILNLILEAIVKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy        716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy        776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
              |||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRHAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy        836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy        896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy        956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        961 RLPNEPFMQSNGYKPAPLDLGAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy       1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy       1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy       1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy       1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db       1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMERDVTHWYTKDQPIFENT 1260

Qy       1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy       1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy       1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy       1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500

Qy       1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db       1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
              ||||||||||||||||||||||||||||||||||:|||| ||||||||||||||||||||
Db       1741 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCMDILELIEMDKLLSFHSHTLTLYAA 1800

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1860

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920

Qy       1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980

Qy       1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1981 PETWDPSFDKGGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2040

Qy       2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091

Db       2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2100

Qy       2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151

Db       2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160

Qy       2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211

Db       2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220

Qy       2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271

Db       2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280

Qy       2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331

Db       2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340

Qy       2332 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391

Db       2341 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400

Qy       2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451

Db       2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460

Qy       2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511

Db       2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520

Qy       2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571

Db       2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580

Qy       2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631

Db       2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640

Qy       2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691

Db       2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700

Qy       2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751

Db       2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760

Qy       2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811

Db       2761 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2820

Qy       2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871

Db       2821 KNYDGEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880

Qy       2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931

Db       2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991

Db       2941 NRSSMRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000

Qy       2992 KKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSD 3051

Db       3001 KKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSD 3060

Qy       3052 TEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSK 3111

Db       3061 TEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSK 3120

Qy       3112 AVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDV 3171

Db       3121 VVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDV 3180

Qy       3172 RITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGT 3231

Db       3181 RITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGT 3240

Qy       3232 HLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASL 3291

Db       3241 HLKTSTSLGYINGVLLPILTAKFDHLANCEYGADPLLDEIQVASYKMLGSLYALGTDASL 3300

Qy       3292 THDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDI 3351

Db       3301 THDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLDKHNQFSLLNRIADHSLEAQDI 3360

Qy       3352 MQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPT 3411

Db       3361 MQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPT 3420

Qy       3412 GGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFL 3471

Db       3421 GGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFL 3480

Qy       3472 PLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYV 3531

Db       3481 PLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYV 3540

Qy       3532 DLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATR 3591

Db       3541 DLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATR 3600

Qy       3592 RVTAVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQ 3651

Db       3601 RVTAVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQ 3660

Qy       3652 HCKDRF-----LKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITV 3706

Db       3661 HCKDRFLKVGTLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITV 3720

Qy       3707 ETAENKAKIIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQT 3766

Db       3721 ETAENKAKIIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQT 3780

Qy       3767 SLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDP 3826

Db       3781 SLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDP 3840

Qy       3827 LTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDE 3886

Db       3841 LTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDE 3900

Qy       3887 GRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGG 3946

Db       3901 GRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGG 3960

Qy       3947 NIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKN 4006

Db       3961 NIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKN 4020

Qy       4007 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFY 4066

Db       4021 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTAAVNVVICTVDYLLRLQESIMDFY 4080

Qy       4067 WHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLF 4126

Db       4081 WHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLF 4140

Qy       4127 LFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASN 4186

Db       4141 LFSHMQDKLSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGKQMVDTLVESASN 4200
```

```
Qy       4187 VELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLAC 4246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 VELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLAC 4260

Qy       4247 CETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYF 4306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYF 4320

Qy       4307 EPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAF 4366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 EPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAF 4380

Qy       4367 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKD 4426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKD 4440

Qy       4427 GVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLL 4486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLL 4500

Qy       4487 GLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITK 4546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITK 4560

Qy       4547 EDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQER 4606
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 EGNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQER 4620

Qy       4607 MEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVL 4666
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       4621 MEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRVVSFLARNFYNLKYVALVL 4680

Qy       4667 AFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVV 4726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 AFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVV 4740

Qy       4727 HIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAE 4786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 HIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAE 4800

Qy       4787 QPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSA 4846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 QPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSA 4860

Qy       4847 QEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLD 4906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 QEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLD 4920

Qy       4907 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNC 4966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNC 4980

Qy       4967 HDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLI 5026
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       4981 HDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISLFFFIIVILLAILQGLI 5040

Qy       5027 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLI 5086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLI 5100

Qy       5087 NKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128
             |||||||||||||||||||||||||||||||||||||||||||
Db       5101 NKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5142
```

RESULT 4
US-10-668-767-146
; Sequence 146, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 5100
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv6
US-10-668-767-146

Query Match 98.9%; Score 26506; DB 4; Length 5100;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 5082; Conservative 5; Mismatches 8; Indels 38; Gaps 3;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||||      |||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720
```

```
Qy       716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
Db       721 YSYGLDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy       776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
Db       781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy       836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
Db       841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy       896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
Db       901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy       956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
Db       961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy      1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
Db      1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy      1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
Db      1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy      1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
Db      1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy      1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
Db      1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy      1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
Db      1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy      1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
Db      1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy      1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
Db      1381 SRPPRKGSMTR-----------GQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1428

Qy      1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
Db      1429 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQSNAQ------- 1481

Qy      1496 PSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1555
Db      1482 -------------MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1527

Qy      1556 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADE 1615
Db      1528 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIIIDDYDRVVENVNRQSCYMVRADE 1587

Qy      1616 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1675
Db      1588 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1647

Qy      1676 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1735
Db      1648 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1707

Qy      1736 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQ 1795
Db      1708 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQ 1767

Qy      1796 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1855
Db      1768 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1827

Qy      1856 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1915
Db      1828 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFV 1887

Qy      1916 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1975
Db      1888 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1947

Qy      1976 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2035
Db      1948 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2007

Qy      2036 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2095
Db      2008 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2067

Qy      2096 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2155
Db      2068 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2127

Qy      2156 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2215
Db      2128 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2187

Qy      2216 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2275
Db      2188 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2247

Qy      2276 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2335
Db      2248 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2307

Qy      2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395
Db      2308 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2367

Qy      2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
Db      2368 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2427

Qy      2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2515
Db      2428 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2487

Qy      2516 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2575
Db      2488 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2547

Qy      2576 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2635
Db      2548 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2607

Qy      2636 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2695
Db      2608 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2667

Qy      2696 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2755
Db      2668 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2727

Qy      2756 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2815
Db      2728 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2787

Qy      2816 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2875
Db      2788 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2847

Qy      2876 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2935
```

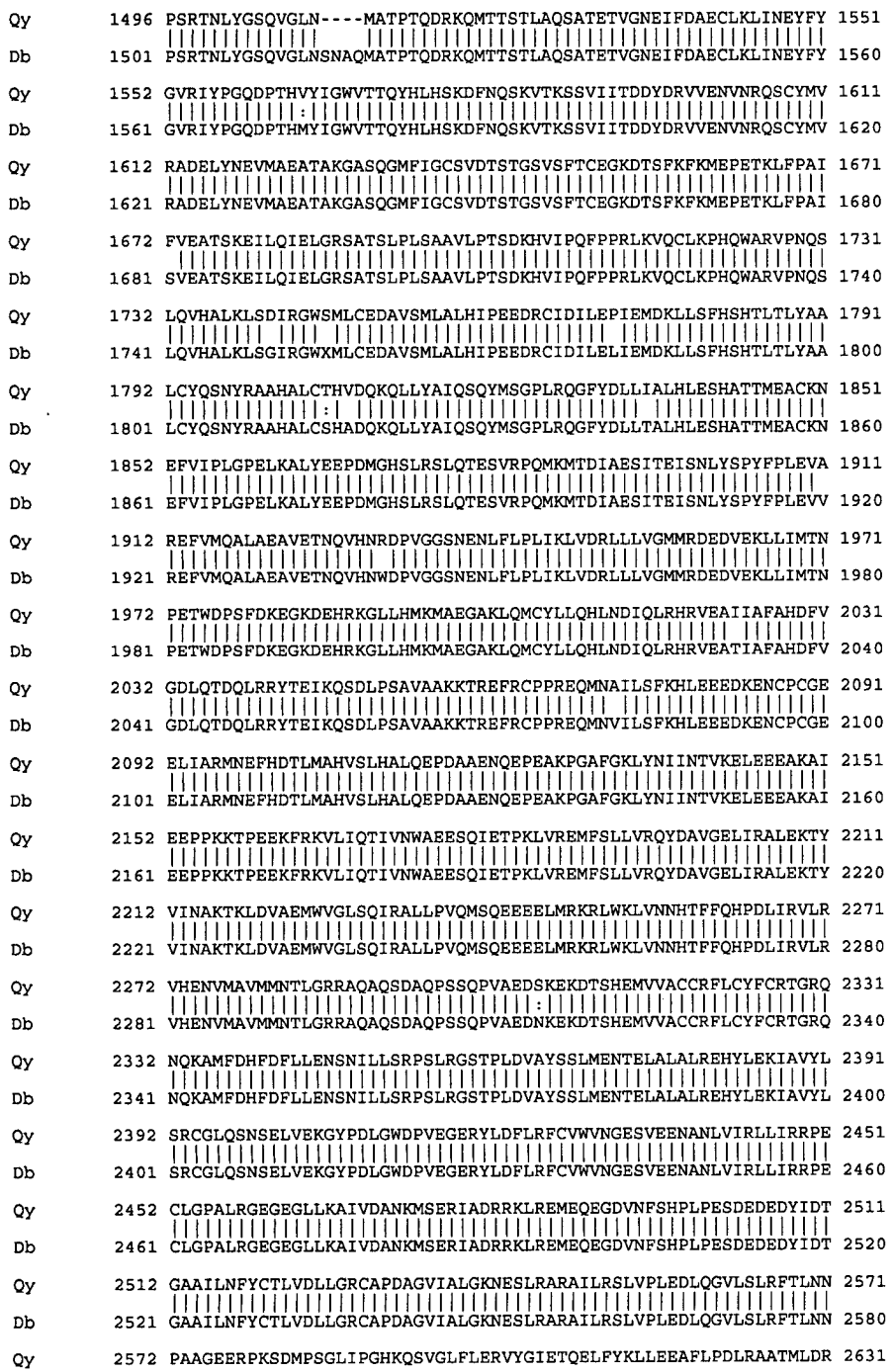
```
Db       2848 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2907
Qy       2936 MRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2995
Db       2908 MRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2967
Qy       2996 EELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQT 3055
Db       2968 EELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQT 3027
Qy       3056 TTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLP 3115
Db       3028 TTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSKVVLP 3087
Qy       3116 LMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITV 3175
Db       3088 LMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITV 3147
Qy       3176 RCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKT 3235
Db       3148 RCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKT 3207
Qy       3236 STSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDR 3295
Db       3208 STSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDR 3267
Qy       3296 KYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKM 3355
Db       3268 KYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKM 3327
Qy       3356 EQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNH 3415
Db       3328 EQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNH 3387
Qy       3416 VTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAE 3475
Db       3388 VTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPLAE 3447
Qy       3476 RVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQR 3535
Db       3448 RVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQR 3507
Qy       3536 NHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTA 3595
Db       3508 NHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTA 3567
Qy       3596 VTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKD 3655
Db       3568 VTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKD 3627
Qy       3656 RFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKI 3715
Db       3628 RFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKI 3687
Qy       3716 IDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHR 3775
Db       3688 IDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHR 3747
Qy       3776 ACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFC 3835
Db       3748 ACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFC 3807
Qy       3836 RGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQE 3895
Db       3808 RGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQE 3867
Qy       3896 MEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGML 3955
Db       3868 MEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGML 3927
Qy       3956 NHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCA 4015
Db       3928 NHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCA 3987
Qy       4016 LFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELI 4075
Db       3988 LFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELI 4047
Qy       4076 DPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKL 4135
Db       4048 DPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKL 4107
Qy       4136 SKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFD 4195
Db       4108 SKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFD 4167
Qy       4196 MFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKL 4255
Db       4168 MFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKL 4227
Qy       4256 DYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEI 4315
Db       4228 DYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEI 4287
Qy       4316 MGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIF 4375
Db       4288 MGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIF 4347
Qy       4376 EMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSL 4435
Db       4348 EMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSL 4407
Qy       4436 SPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTD 4495
Db       4408 SPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTD 4467
Qy       4496 EPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVK 4555
Db       4468 EPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVPAFGLDITKEDNGQIQVK 4527
Qy       4556 PHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQA 4615
Db       4528 PHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQA 4587
Qy       4616 AMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLL 4675
Db       4588 AMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLL 4647
Qy       4676 FYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYM 4735
Db       4648 FYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYM 4707
Qy       4736 EHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKS 4795
Db       4708 EHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAERPEDDDLKS 4767
Qy       4796 HWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGL 4855
Db       4768 HWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGL 4827
Qy       4856 IHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLR 4915
Db       4828 IHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLR 4887
Qy       4916 TILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVF 4975
Db       4888 TILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVF 4947
Qy       4976 NLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRD 5035
Db       4948 NLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRD 5007
Qy       5036 QLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTG 5095
Db       5008 QLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTG 5067
```

```
Qy       5096 QETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128
             ||||||||||||||||||||||||||||||||||
Db       5068 QETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5100
```

RESULT 5
US-10-668-767-2
; Sequence 2, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 5142
;   TYPE: PRT
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1755)..(1755)
;   OTHER INFORMATION: Xaa = Ser
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4250)..(4250)
;   OTHER INFORMATION: Xaa = Thr
US-10-668-767-2

  Query Match 98.8%; Score 26469; DB 4; Length 5142;
  Best Local Similarity 98.7%; Pred. No. 0;
  Matches 5074; Conservative 18; Mismatches 36; Indels 14; Gaps 3;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              |||||||||||||||| ||||||||:|||||||||||||| ||||||||||||||||||
Db          1 MAEAEGGASEQDDVSILRTEDMVCMSCTATGERVCLAAEGLGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||     |||||||:||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGYRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVAIERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYKGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEPTTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDLSRSQEEESMTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLTNYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        481 DLFQEEGILNLILEAIDKINVVTSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
              |||||||||| ||||||||||||||||||||||:||||||||||||||||||||||||||
Db        541 TNCAQFANSNRFNWLFSRLGSQASGEGTGMLDVLHCILIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy        716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy        776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy        836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy        896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy        956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVGQLAENTHNLWARERIQQGWTYGLNED 1020

Qy       1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy       1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy       1136 EEKVYSGNTESPGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 EEKVYSGNTESPGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy       1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy       1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy       1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
              |||||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1321 RRWVEIKDRQRILMKEAVEAQMSAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy       1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy       1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500
```


Qy 1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1561 GVRIYPGQDPTHMYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1681 SVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1741 LQVHALKLSGIRGWXMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAA 1800
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1801 LCYQSNYRAAHALCSHADQKQLLYAIQSQYMSGPLRQGFYDLLTALHLESHATTMEACKN 1860
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1921 REFVMQALAEAVETNQVHNWDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1981 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEATIAFAHDFV 2040
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNVILSFKHLEEEDKENCPCGE 2100
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151
Db 2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160
Qy 2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211
Db 2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220
Qy 2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271
Db 2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280
Qy 2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331
Db 2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340
Qy 2332 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391
Db 2341 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400
Qy 2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451
Db 2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460
Qy 2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
Db 2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520
Qy 2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571
Db 2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580
Qy 2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631
Db 2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLGRVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640
Qy 2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691
Db 2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700
Qy 2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751
Db 2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760
Qy 2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811
Db 2761 GAGQGAFGASSDEEKRLTMMLFSSIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYTLS 2820
Qy 2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871
Db 2821 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880
Qy 2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931
Db 2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940
Qy 2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
Db 2941 NRSSMGRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000
Qy 2992 KKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSD 3051
Db 3001 KKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSD 3060
Qy 3052 TEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSK 3111
Db 3061 TEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFSK 3120
Qy 3112 AVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDV 3171
Db 3121 VVLPLMEKYFSTHRNYFIAVATATNSVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDV 3180
Qy 3172 RITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGT 3231
Db 3181 RITVRCLQVLVRGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGT 3240
Qy 3232 HLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASL 3291
Db 3241 HLKTSTSLGYIHGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASL 3300
Qy 3292 THDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDI 3351
Db 3301 THDRKYLKTEIERHKPALGSCLGAFSSTFPVAFQEPHLNKHNQFSLLNRIADHSLEAQDI 3360
Qy 3352 MQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPT 3411
Db 3361 MQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPT 3420
Qy 3412 GGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFL 3471
Db 3421 GGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFL 3480
Qy 3472 PLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYV 3531
Db 3481 PLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKYV 3540
Qy 3532 DLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATR 3591
Db 3541 DLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATR 3600
Qy 3592 RVTAVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQ 3651
Db 3601 RVTAVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQ 3660
Qy 3652 HCKDRF-----LKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITV 3706

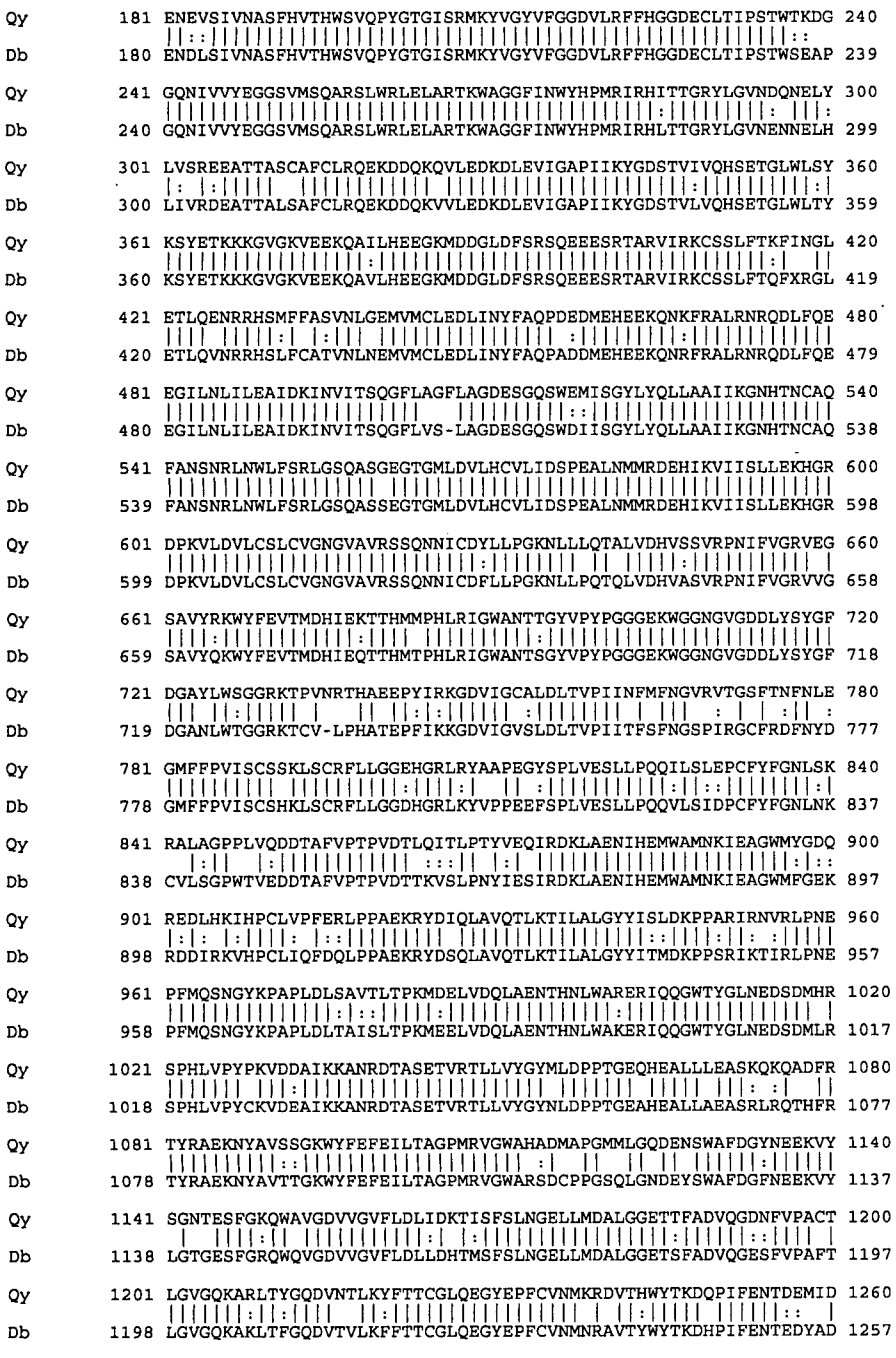
```
Db       3661 HCKDRFLKVGTLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITV 3720

Qy       3707 ETAENKAKIIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQT 3766

Db       3721 ETAENKAKIIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFRQT 3780

Qy       3767 SLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVEEGEKPDP 3826

Db       3781 SLHSLPRHRACNIFARTYYELWLEEENIRQEVMIEDLTQSFEDAELKKSDVVEEGEKPDP 3840

Qy       3827 LTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDE 3886

Db       3841 LTQLVTTSCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGGEAEAEDE 3900

Qy       3887 GRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGG 3946

Db       3901 GRASIHEQEMEKQKLLFHQARPADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGG 3960

Qy       3947 NIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKN 4006

Db       3961 NIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLEGAAGEKN 4020

Qy       4007 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFY 4066

Db       4021 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFY 4080

Qy       4067 WHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLF 4126

Db       4081 WHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLF 4140

Qy       4127 LFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASN 4186

Db       4141 LFSHMQDKLSKHSSQVDLLKELLNPQKDMITMMLSMLEGNVVNGTIVKQMVDTLVGSASN 4200

Qy       4187 VELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLAC 4246

Db       4201 VELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYXPEEIEFLLAC 4260

Qy       4247 CETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYF 4306

Db       4261 CETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLDYF 4320

Qy       4307 EPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDKEKLEAF 4366

Db       4321 EPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGDREKLEAF 4380

Qy       4367 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKD 4426

Db       4381 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDGDERAGKDPFRRGLQSVKD 4440

Qy       4427 GVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLL 4486

Db       4441 GVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYPFYYLGYGVLVVVRYIFGVLL 4500

Qy       4487 GLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITK 4546

Db       4501 GLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITK 4560

Qy       4547 EDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQER 4606

Db       4561 EDNGQIQVKPHESPSTSTPSSGGEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQER 4620

Qy       4607 MEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVL 4666

Db       4621 MEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVL 4680

Qy       4667 AFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVV 4726

Db       4681 AFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGETGEDDDALEVV 4740

Qy       4727 HIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAE 4786

Db       4741 HIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAE 4800
```

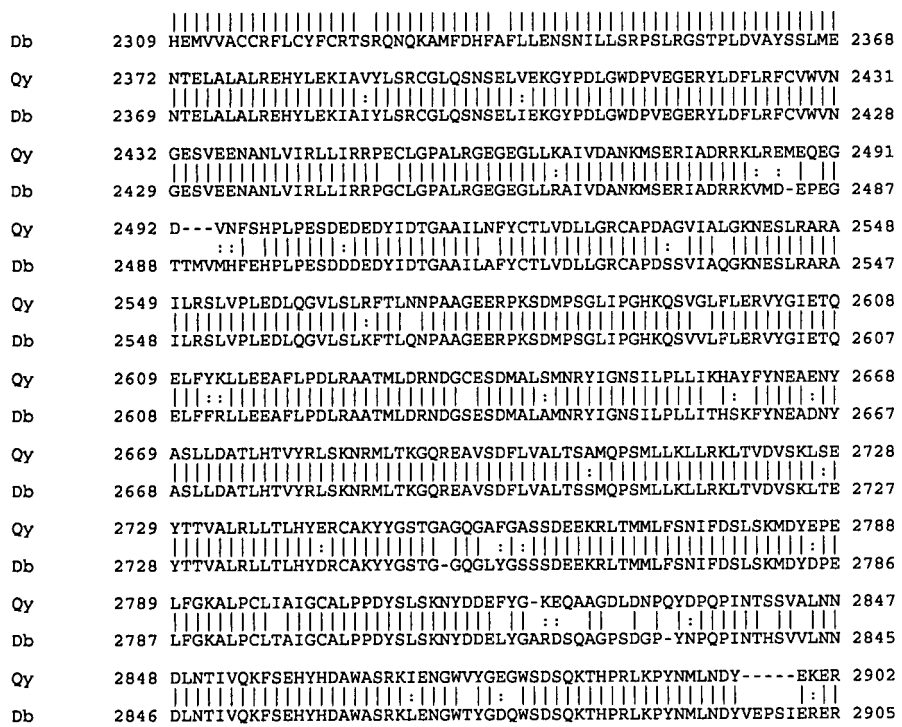
```
Qy       4787 QPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSA 4846

Db       4801 QPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSA 4860

Qy       4847 QEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLD 4906

Db       4861 QEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLD 4920

Qy       4907 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNC 4966

Db       4921 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQGEDDEVNRNC 4980

Qy       4967 HDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLI 5026

Db       4981 HDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLI 5040

Qy       5027 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLI 5086

Db       5041 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLI 5100

Qy       5087 NKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5128

Db       5101 NKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMGE 5142
```

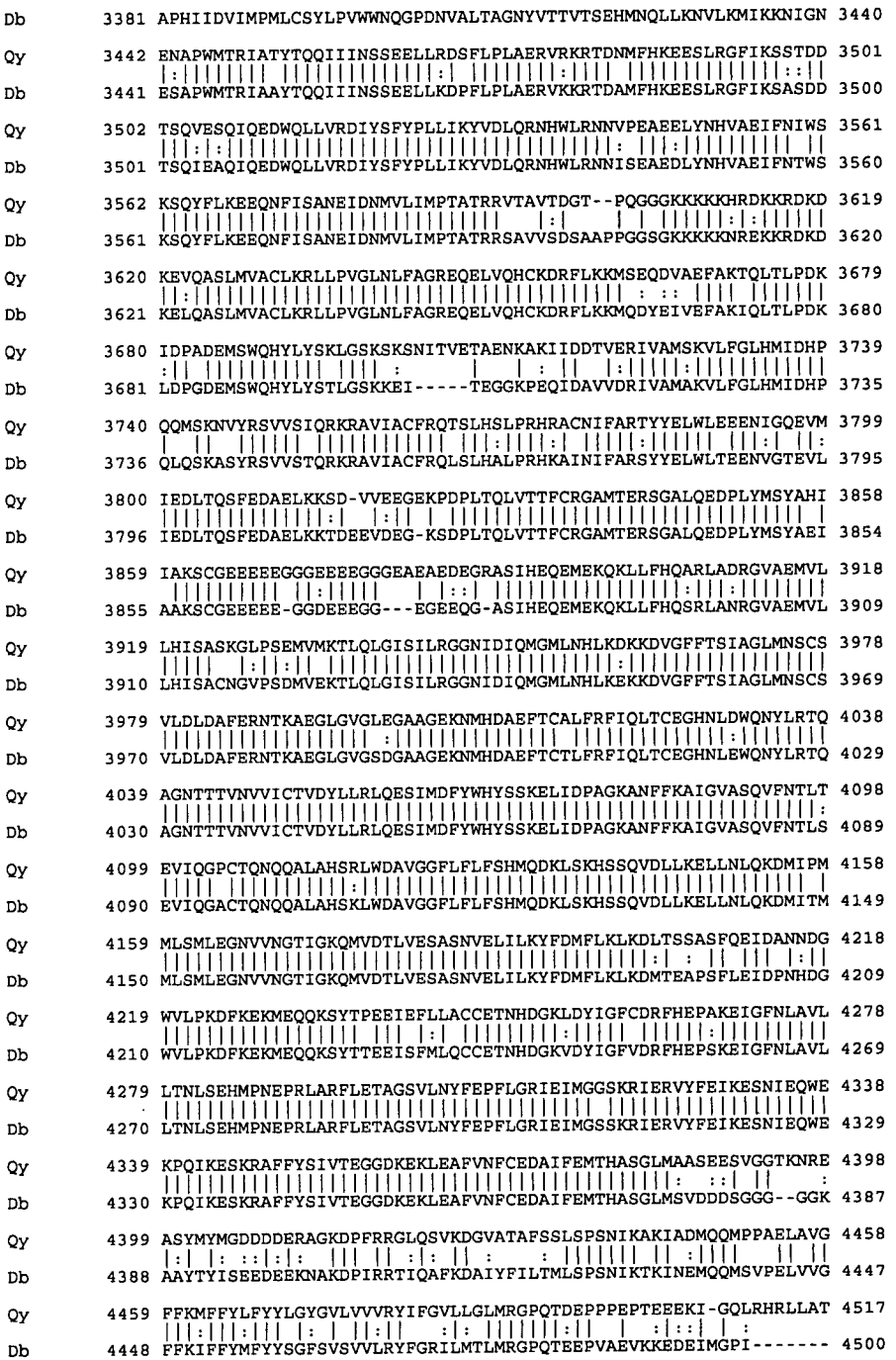
RESULT 6
US-10-668-767-8
; Sequence 8, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5127
; TYPE: PRT
; ORGANISM: Peregrinus maidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (416)..(416)
; OTHER INFORMATION: Xaa = Ile
US-10-668-767-8

Query Match 80.7%; Score 21630; DB 4; Length 5127;
Best Local Similarity 80.3%; Pred. No. 0;
Matches 4174; Conservative 396; Mismatches 484; Indels 142; Gaps 46;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Db          1 MADSEGG-SEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Db         60 STCVFVIEQALSVRALQELVTAAGSEEGKGTGSGHRTLLYGNAILLRHQNSDMYLACSST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179
```


Qy 181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db 180 ENDLSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSEAP 239
Qy 241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db 240 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHLTTGRYLGVNENNELH 299
Qy 301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db 300 LIVRDEATTALSAFCLRQEKDDQKVVLEDKDLEVIGAPIIKYGDSTVLVQHSETGLWLTY 359
Qy 361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db 360 KSYETKKKGVGKVEEKQAVLHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTQFXRGL 419
Qy 421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db 420 ETLQVNRRHSLFCATVNLNEMVMCLEDLINYFAQPADDMEHEEKQNRFRALRNRQDLFQE 479
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 480 EGILNLILEAIDKINVITSQGFLVS-LAGDESGQSWDIISGYLYQLLAAIIKGNHTNCAQ 538
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 539 FANSNRLNWLFSRLGSQASSEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLPQTQLVDHVASVRPNIFVGRVVG 658
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 659 SAVYQKWYFEVTMDHIEQTTHMTPHLRIGWANTSGYVPYPGGGEKWGGNGVGDDLYSYGF 718
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 719 DGANLWTGGRKTCV-LPHATEPFIKKGDVIGVSLDLTVPIITFSFNGSPIRGCFRDFNYD 777
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 778 GMFFPVISCSHKLSCRFLLGGDHGRLKYVPPEEFSPLVESLLPQQVLSIDPCFYFGNLNK 837
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 838 CVLSGPWTVEDDTAFVPTPVDTTKVSLPNYIESIRDKLAENIHEMWAMNKIEAGWMFGEK 897
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 898 RDDIRKVHPCLIQFDQLPPAEKRYDSQLAVQTLKTILALGYYITMDKPPSRIKTIRLPNE 957
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 958 PFMQSNGYKPAPLDLTAISLTPKMEELVDQLAENTHNLWAKERIQQGWTYGLNEDSDMLR 1017
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1018 SPHLVPYCKVDEAIKKANRDTASETVRTLLVYGYNLDPPTGEAHEALLAEASRLRQTHFR 1077
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1078 TYRAEKNYAVTTGKWYFEFEILTAGPMRVGWARSDCPPGSQLGNDEYSWAFDGFNEEKVY 1137
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
Db 1138 LGTGESFGRQWQVGDVVGVFLDLLDHTMSFSLNGELLMDALGGETSFADVQGESFVPAFT 1197
Qy 1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
Db 1198 LGVGQKAKLTFGQDVTVLKFFTTCGLQEGYEPFCVNMNRAVTYWYTKDHPIFENTEDYAD 1257
Qy 1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
Db 1258 SRIDVTRIPAGSDTPPCLKISHNLFESMEKANWEFLRLSLPVICHSSFIEESEKLKRWQE 1317
Qy 1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH--YEDN--------QEELPSSK 1370
Db 1318 IRIRQHRLLVEA-DQTTPAHMEQIMKSGLSMSDIKGLHRGYSEDAVEADEMMMQSTPTTK 1376
Qy 1371 MK-RLPSRPPRKGSMTRGVTIQNYNNLQPGQVNG------MHRSTSEAEMAKYDLGAQGL 1423
Db 1377 SKMRQPSRPPRKGSLSR--------NEDMPMINGSLEQSKMNRSTSELDLNRYNADLQN- 1427
Qy 1424 TPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPN-----P 1478
Db 1428 DKDDKK-KRGRSPFRFFSRKREASNER--SKKAKSPEPNSMMEADRGQMGRSQHHMMRTP 1484
Qy 1479 QIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIF 1538
Db 1485 TVKVTAPDMKVIPPTI-PERSNM--------------PKQMTGAPLSGSGIESVGNEIF 1528
Qy 1539 DAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDR 1598
Db 1529 DGECLKLINEYFYGVRIFPGQDPTHVYVGWVTTQYHFFANEFNQSKVRKVTVHTLDEFSR 1588
Qy 1599 VVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFK 1658
Db 1589 VNESVDRQSCYMVRSDELFNEVTNDSSGKGASQGMFIGCFVDAATGYISFTCEGKETSHK 1648
Qy 1659 FKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQC 1718
Db 1649 FKMEPETKLFPAIFVEATSKEILQIELGRTSTTLPLSAAVLQNSERHVNPQFPPRLKVQC 1708
Qy 1719 LKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKL 1778
Db 1709 LKPHQWARVPNVSLQVHALKLSDIRGWSMLCEDPMSMLALHIPEEDRSIDILELIEMEKL 1768
Qy 1779 LSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALH 1838
Db 1769 LSFHAHTLTLYAALCFQSNYRAAHTLCSHVDEKQLLYAIRSDYMSGPLRQGFYDLLIALH 1828
Qy 1839 LESHATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIA------ 1892
Db 1829 LESHAYTMEVCKNEFIIPIGQELKDVYEDPEMCHSLRSLKTESVLPTMKMTDKADEPSPS 1888
Qy 1893 ESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRL 1952
Db 1889 EVVDNIRSLYSPQFPLDVVRDFVMAALDEAVQINQLHNRDPVGGSNENYFLPLLKLVDRL 1948
Qy 1953 LLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLN 2012
Db 1949 LLVGMLRDGDVMKLLIMFSPETWDTAFEKDGKDEHRKGLLTMKMAEGAKLQMCYLLHHLY 2008
Qy 2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNA 2072
Db 2009 DIQLRHRVEAIISFSVDFVGDLQSDQLRRYIEIKQSDLPSAIAAKKTREFRCPPREQMNA 2068
Qy 2073 ILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-NQEPEAKPGAF 2131
Db 2069 ILGFKNLEEGDIENCPCGDELRERLNSFHEKLMHKVSLLALQEPSEEEASAEEVKKPNAL 2128
Qy 2132 GKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFS 2191
Db 2129 NRLYNFINAVKELEETPQIEEEPEKKTPEEIFRKVLISTIVKWAEETQIESPKLVREMFS 2188
Qy 2192 LLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRL 2251
Db 2189 LLVRQYDTVGELIRALGKTYVINSKTKDDAALMWVGLSQIRALLPVQMSQEEEGLMRERL 2248
Qy 2252 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTS 2311
Db 2249 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAPQAGQEGEPVAKEKDTS 2308
Qy 2312 HEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLME 2371


Db 2309 HEMVVACCRFLCYFCRTSRQNQKAMFDHFAFLLENSNILLSRPSLRGSTPLDVAYSSLME 2368
Qy 2372 NTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVN 2431
Db 2369 NTELALALREHYLEKIAIYLSRCGLQSNSELIEKGYPDLGWDPVEGERYLDFLRFCVWVN 2428
Qy 2432 GESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEG 2491
Db 2429 GESVEENANLVIRLLIRRPGCLGPALRGEGEGLLRAIVDANKMSERIADRRKVMD-EPEG 2487
Qy 2492 D---VNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARA 2548
Db 2488 TTMVMHFEHPLPESDDDEDYIDTGAAILAFYCTLVDLLGRCAPDSSVIAQGKNESLRARA 2547
Qy 2549 ILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQ 2608
Db 2548 ILRSLVPLEDLQGVLSLKFTLQNPAAGEERPKSDMPSGLIPGHKQSVVLFLERVYGIETQ 2607
Qy 2609 ELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENY 2668
Db 2608 ELFFRLLEEAFLPDLRAATMLDRNDGSESDMALAMNRYIGNSILPLLITHSKFYNEADNY 2667
Qy 2669 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSE 2728
Db 2668 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSSMQPSMLLKLLRKLTVDVSKLTE 2727
Qy 2729 YTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPE 2788
Db 2728 YTTVALRLLTLHYDRCAKYYGSTG-GQGLYGSSSDEEKRLTMMLFSNIFDSLSKMDYDPE 2786
Qy 2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQPINTSSVALNN 2847
Db 2787 LFGKALPCLTAIGCALPPDYSLSKNYDDELYGARDSQAGPSDGP-YNPQPINTHSVVLNN 2845
Qy 2848 DLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDY-----EKER 2902
Db 2846 DLNTIVQKFSEHYHDAWASRKLENGWTYGDQWSDSQKTHPRLKPYNMLNDYVEPSIERER 2905
Qy 2903 YKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPH 2962
Db 2906 YKEPVRESIKALLAIGWTVEHSEADVPLTSRGSIRRQSK-----PNAMVDSSTPFNYHPN 2960
Qy 2963 PVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKK 3022
Db 2961 PIDMTNLTLGREMQNMAERLAENAHDIWAKKKKEELITCGGGIHPQLVPYDLLTDKEKKK 3020
Qy 3023 DRERSQEFLKYLQYQGYKLHRPSK-APQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRAT 3081
Db 3021 DRERSQEFLKYLQYQGYKLHRPSRTGGPSESEQLAAQATGELRFAYSLLEKLIQYIDRAS 3080
Qy 3082 INMKLLKPSTTFSRRSSFKTSTRDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAA 3141
Db 3081 INMKLLKPSTTFSRRSSFKTCTRDIKFFSKVVLPLVEKYFSTHRNYFIAVATASNNIGAA 3140
Qy 3142 SLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTS 3201
Db 3141 SLKEKEMVASLFCKLANLLRSRLAAFGADVRISVKCLQVLVKGIDAKSLVKNCPEFIRTS 3200
Qy 3202 MLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCE 3261
Db 3201 MLTFFNNTADDLGHTIQNLQEGKYSHLRGAHLKTSTSLFYINDVILPVLTAMFDHLAACE 3260
Qy 3262 YGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFP 3321
Db 3261 YGSDLVLDEIQVASYKMLGSLYTLGIDVTLTHDRKYLKTEIDRHRPQLGRCLGAYASTFP 3320
Qy 3322 VAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCMPTLETILGEVDQFVESDKTYNE 3381
Db 3321 VAFLEPHLNKHNQFSLVNRIADHSLEAQDILSRMESTMPTLDNILSEVDQFVESDKTHND 3380
Qy 3382 APHIIDVVLPLLCSYLPFWWAQGPDNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGN 3441

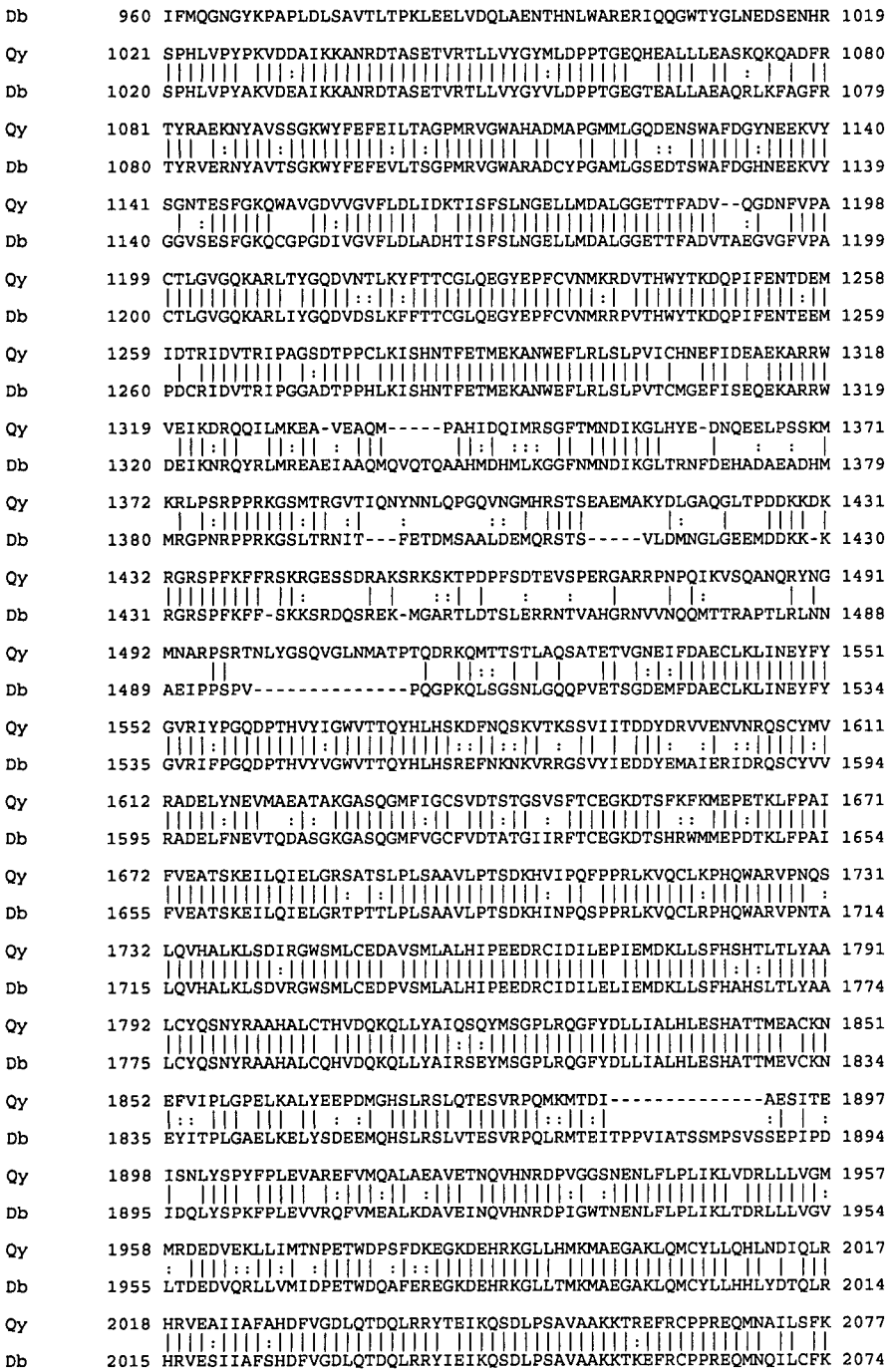

Db 3381 APHIIDVIMPMLCSYLPVWWNQGPDNVALTAGNYVTTVTSEHMNQLLKNVLKMIKKNIGN 3440
Qy 3442 ENAPWMTRIATYTQQIIINSSEELLRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDD 3501
Db 3441 ESAPWMTRIAAYTQQIIINSSEELLKDPFLPLAERVKKRTDAMFHKEESLRGFIKSASDD 3500
Qy 3502 TSQVESQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWS 3561
Db 3501 TSQIEAQIQEDWQLLVRDIYSFYPLLIKYVDLQRNHWLRNNISEAEDLYNHVAEIFNTWS 3560
Qy 3562 KSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTDGT--PQGGGKKKKKHRDKKRDKD 3619
Db 3561 KSQYFLKEEQNFISANEIDNMVLIMPTATRRSAVVSDSAAPPGGSGKKKKKNREKKRDKD 3620
Qy 3620 KEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDK 3679
Db 3621 KELQASLMVACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMQDYEIVEFAKIQLTLPDK 3680
Qy 3680 IDPADEMSWQHYLYSKLGSKSKSNITVETAENKAKIIDDTVERIVAMSKVLFGLHMIDHP 3739
Db 3681 LDPGDEMSWQHYLYSTLGSKKEI-----TEGGKPEQIDAVVDRIVAMAKVLFGLHMIDHP 3735
Qy 3740 QQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEVM 3799
Db 3736 QLQSKASYRSVVSTQRKRAVIACFRQLSLHALPRHKAINIFARSYYELWLTEENVGTEVL 3795
Qy 3800 IEDLTQSFEDAELKKSD-VVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHI 3858
Db 3796 IEDLTQSFEDAELKKTDEEVDEG-KSDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAEI 3854
Qy 3859 IAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVL 3918
Db 3855 AAKSCGEEEEE-GGDEEEGG---EGEEQG-ASIHEQEMEKQKLLFHQSRLANRGVAEMVL 3909
Qy 3919 LHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCS 3978
Db 3910 LHISACNGVPSDMVEKTLQLGISILRGGNIDIQMGMLNHLKEKKDVGFFTSIAGLMNSCS 3969
Qy 3979 VLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQ 4038
Db 3970 VLDLDAFERNTKAEGLGVGSDGAAGEKNMHDAEFTCTLFRFIQLTCEGHNLEWQNYLRTQ 4029
Qy 4039 AGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLT 4098
Db 4030 AGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLS 4089
Qy 4099 EVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPM 4158
Db 4090 EVIQGACTQNQQALAHSKLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITM 4149
Qy 4159 MLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDG 4218
Db 4150 MLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDMTEAPSFLEIDPNHDG 4209
Qy 4219 WVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVL 4278
Db 4210 WVLPKDFKEKMEQQKSYTTEEISFMLQCCETNHDGKVDYIGFVDRFHEPSKEIGFNLAVL 4269
Qy 4279 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWE 4338
Db 4270 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGSSKRIERVYFEIKESNIEQWE 4329
Qy 4339 KPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNRE 4398
Db 4330 KPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMSVDDDSGGG--GGK 4387
Qy 4399 ASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVG 4458
Db 4388 AAYTYISEEDEEKNAKDPIRRTIQAFKDAIYFILTMLSPSNIKTKINEMQQMSVPELVVG 4447
Qy 4459 FFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKI-GQLRHRLLAT 4517
Db 4448 FFKIFFYMFYYSGFSVSVVLRYFGRILMTLMRGPQTEEPVAEVKKEDEIMGPI------- 4500

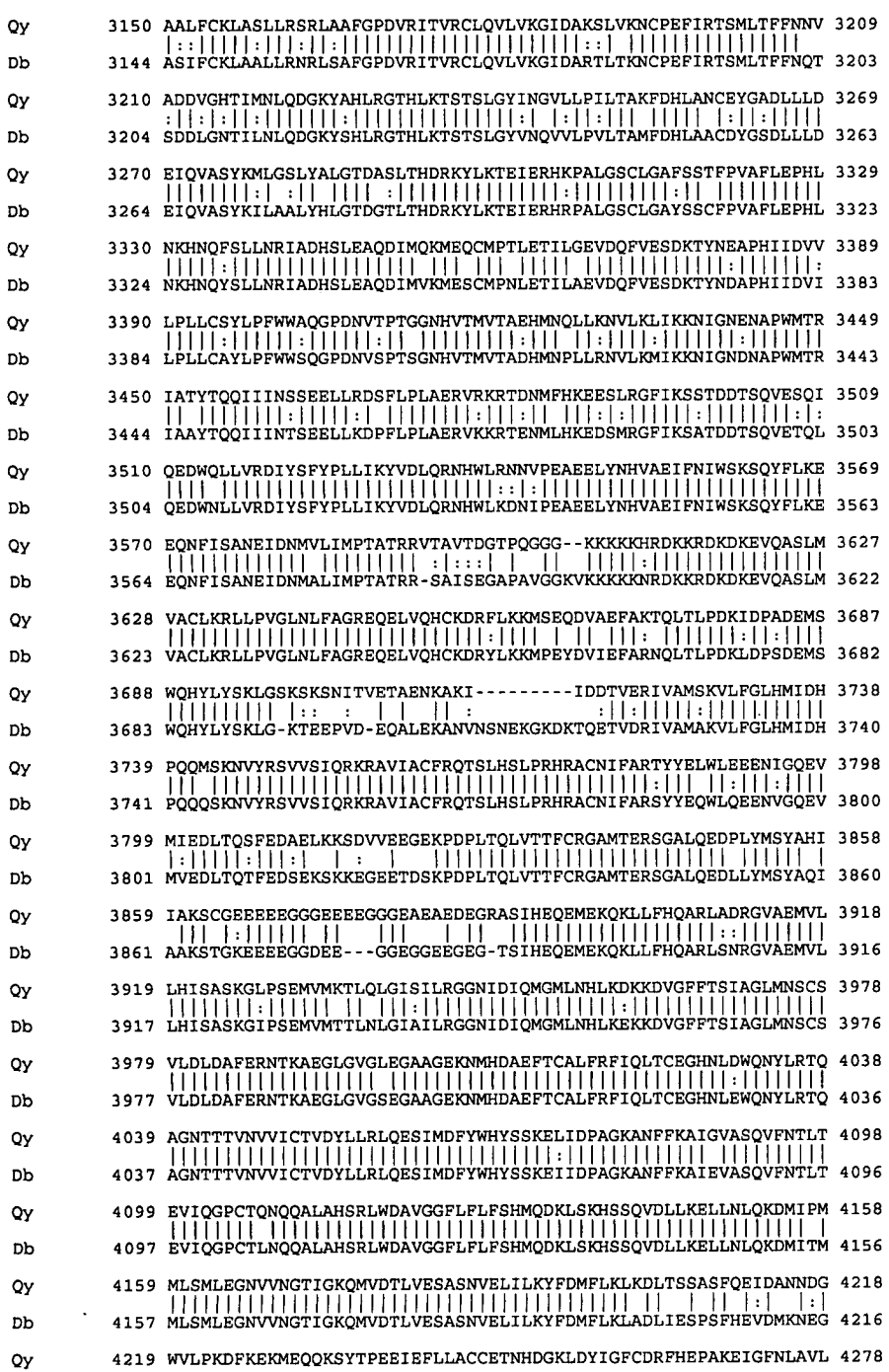
```
Qy       4518 QSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESPST-STPSSGEE------ 4570
Db       4501 ---RALP--PPPPDNKEASSSS-----AKDDSG--QAKPADGGATLALTASGEEHKEGGA 4548

Qy       4571 ----AEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKK 4626
Db       4549 TEEGAEDGAKPEGAETTEGTTMTLADLLGGEAARKEAVARAEVAAEQQAVMAAVEAEAKH 4608

Qy       4627 AVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTL---- 4682
Db       4609 EVVS-EPSAFSQIDFNRYTHRAVSFLARNFYNLKYVALVLAFCINFILLFYKVTTLGEDE 4667

Qy       4683 -DGEGGE-GSGLGDII---AGGGSG-SGAGSGSGDGSGESGED-----DDALEVVHIDED 4731
Db       4668 DDGGSGELGGGLAEDLLEELGGGSGEEGGGLSGGISGGESGEDGSGEEEDPIELVHVNED 4727

Qy       4732 FFYMEHVIKMAAVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDD 4791
Db       4728 FFYMAHVMKIAAMLHSLVSLAMLIAYYHLKVPLAIFKREKEIARRLEFDGLYIAEQPEDD 4787

Qy       4792 DLKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEG 4851
Db       4788 DIKSHWDKLVISAKSFPVNYWDKFVKKKVRQKYSETYDFDSISTLLGMEKTSFSSQETEE 4847

Qy       4852 SKGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGF 4911
Db       4848 GTGIINFILNIDWRYQVWKAGVTITDNAFLYSLWYFIFSILGNFNNFFFAAHLLDVAVGF 4907

Qy       4912 KTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLT 4971
Db       4908 KTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDEEVDKKCHDMLT 4967

Qy       4972 CFVFNLYKGVRAGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFG 5031
Db       4968 CFVFHLYKGVRAGSGIGDEIEPPDGDDYEVYRIMFDITFFFFVIVILLAIIQGLIIDAFG 5027

Qy       5032 ELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDT 5091
Db       5028 ELRDQLESVKEDMESNCFICGIGKDYFDKVPHGFDTHVQQEHNLANYMFFLMHLINKPDT 5087

Qy       5092 EYTGQETYVWNMYTQRCWDFFPVGDCFRKQYEDLMG 5127
Db       5088 EYTGQETYVWNMYQQRCWDFFPVGDCFRKQYEDELG 5123
```

RESULT 7
US-10-668-767-122
; Sequence 122, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 5127
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: gi 17352469
US-10-668-767-122

Query Match 79.9%; Score 21403; DB 4; Length 5127;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 4101; Conservative 439; Mismatches 520; Indels 122; Gaps 41;

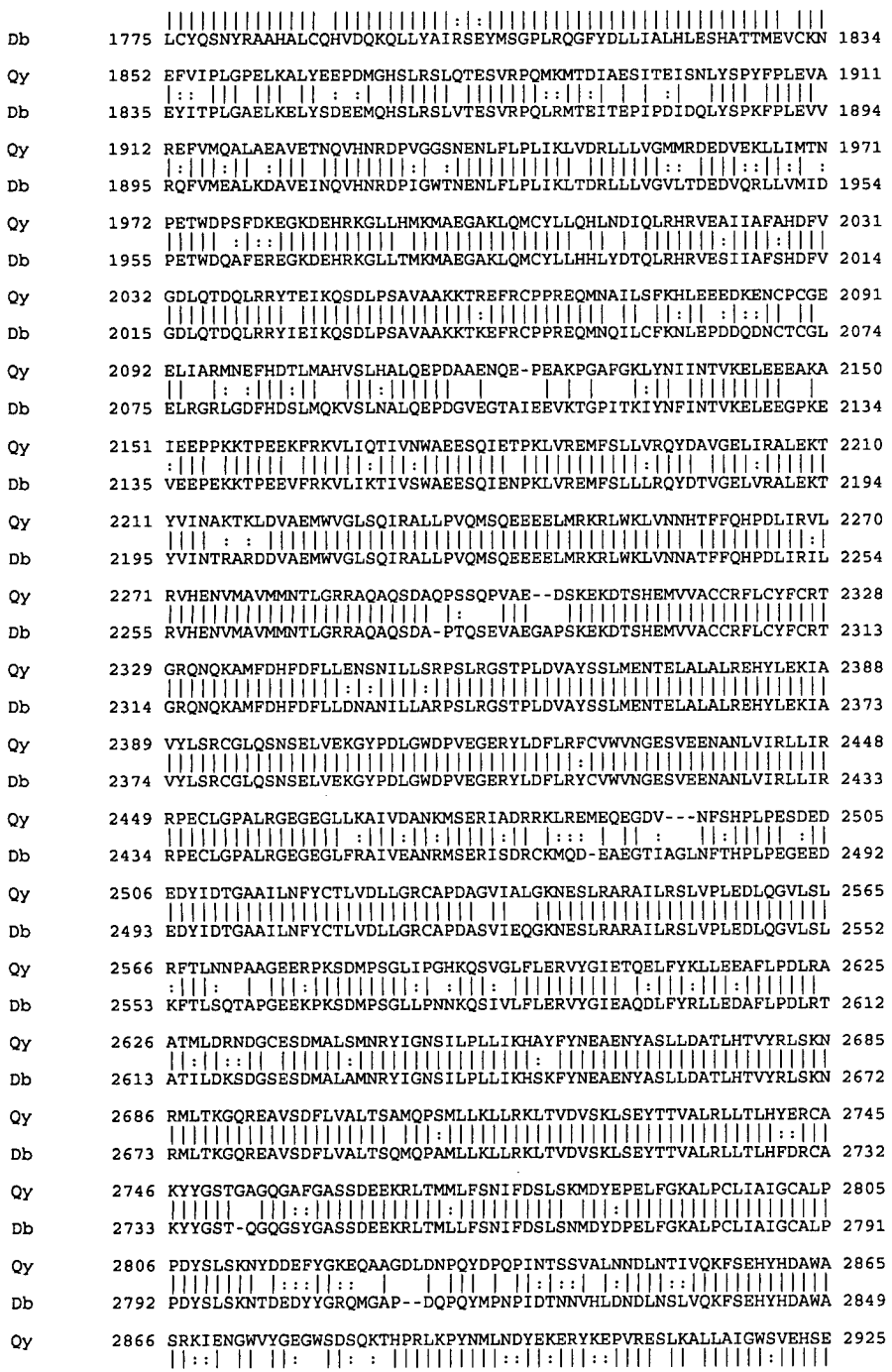
```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db        900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
```


Db 960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1140 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1894
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1895 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1954
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1955 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2014
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2015 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2074
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2075 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2134
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2135 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2194
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2195 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2254
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2255 NATFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2313
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2314 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2373
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2374 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2433
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2434 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2492
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2493 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILR 2552
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2553 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2612
Qy 2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db 2613 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2672
Qy 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db 2673 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2732
Qy 2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db 2733 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2791
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
Db 2792 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2849
Qy 2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db 2850 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2909
Qy 2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
Db 2910 KGLLAIGWTVEHSEVEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2964
Qy 2970 TLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQE 3029
Db 2965 TLSREMQNMAERLAENSHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQE 3024
Qy 3030 FLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKP 3089
Db 3025 FLKYMQYQGYKLHKPSKGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKP 3083
Qy 3090 STTFSRRSSFKTSTRDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMV 3149
Db 3084 STTFSRRSSFKTATRDIKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMV 3143



RESULT 8
US-10-668-767-121
; Sequence 121, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James

```
; APPLICANT:  Smith, Rejane
; APPLICANT:  Tao, Yong
; APPLICANT:  Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE:  2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
;   LENGTH: 5113
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: gi 17352467
US-10-668-767-121

  Query Match            79.8%;  Score 21376;  DB 4;  Length 5113;
  Best Local Similarity  79.1%;  Pred. No. 0;
  Matches 4090;  Conservative  447;  Mismatches  523;  Indels  108;  Gaps   40;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db        900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db        960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db       1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db       1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db       1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db       1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db       1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db       1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379

Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db       1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db       1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db       1489 AEIPPSPV-------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db       1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db       1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db       1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db       1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
```

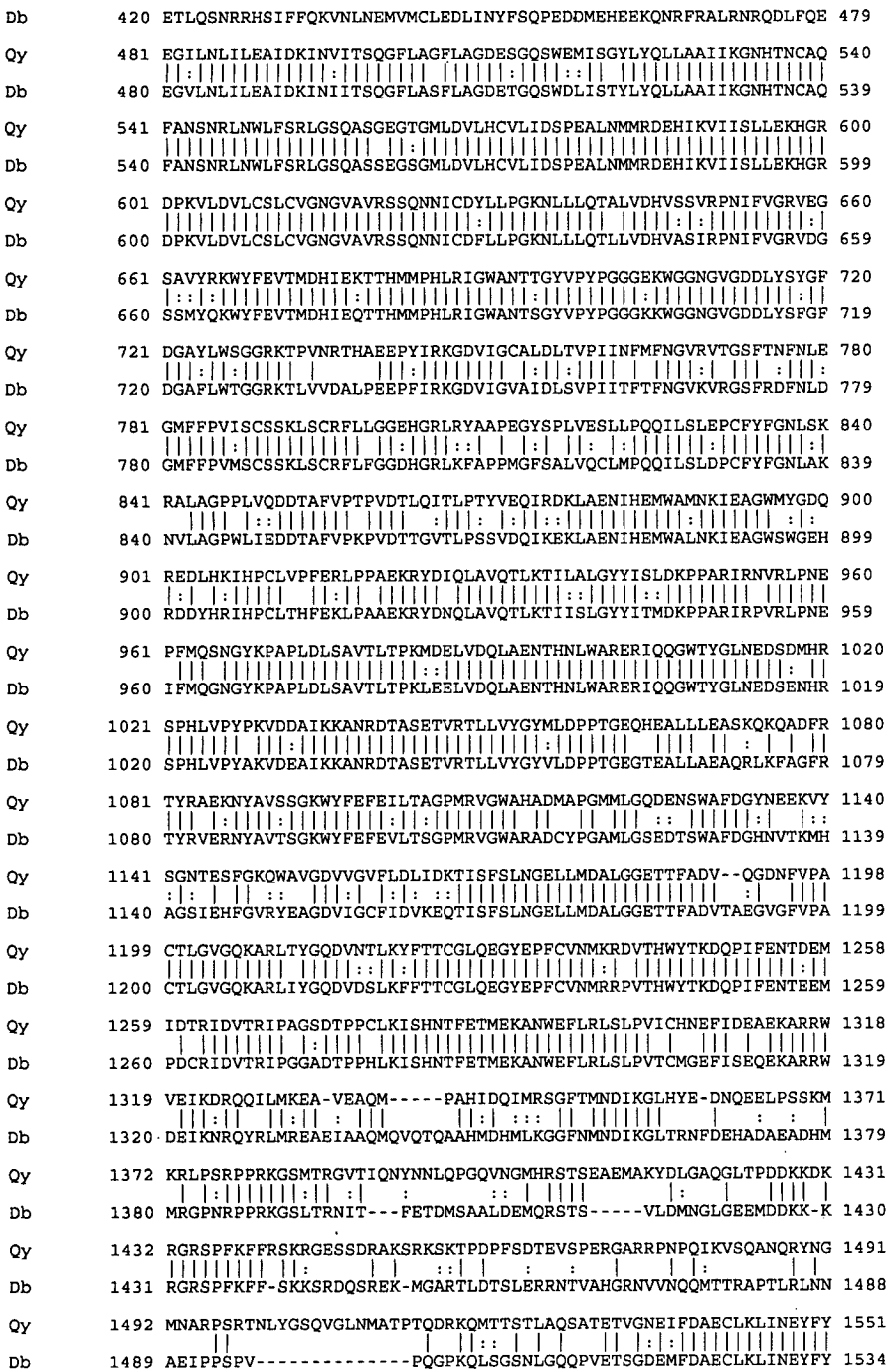

Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1894
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1895 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1954
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1955 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFV 2014
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2015 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2074
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
Db 2075 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2134
Qy 2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db 2135 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2194
Qy 2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db 2195 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2254
Qy 2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db 2255 RVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2313
Qy 2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db 2314 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2373
Qy 2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db 2374 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIR 2433
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db 2434 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2492
Qy 2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db 2493 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSL 2552
Qy 2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db 2553 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2612
Qy 2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
Db 2613 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2672
Qy 2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db 2673 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2732
Qy 2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db 2733 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2791
Qy 2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db 2792 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2849
Qy 2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db 2850 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2909
Qy 2926 VDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLA 2983
Db 2910 VEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLA 2964
Qy 2984 DNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHR 3043
Db 2965 ENSHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQEFLKYMQYQGYKLHK 3024
Qy 3044 PSKAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTST 3103
Db 3025 PSKGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKPSTTFSRRSSFKTAT 3083
Qy 3104 RDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSR 3163
Db 3084 RDIKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMVASIFCKLAALLRNR 3143
Qy 3164 LAAFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDG 3223
Db 3144 LSAFGPDVRITVRCLQVLVKGIDARTLTKNCPEFIRTSMLTFFNQTSDDLGNTILNLQDG 3203
Qy 3224 KYAHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLY 3283
Db 3204 KYSHLRGTHLKTSTSLGYVNQVVLPVLTAMFDHLAACDYGSDLLLDEIQVASYKILAALY 3263
Qy 3284 ALGTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIAD 3343
Db 3264 HLGTDGTLTHDRKYLKTEIERHRPALGSCLGAYSSCFPVAFLEPHLNKHNQYSLLNRIAD 3323
Qy 3344 HSLEAQDIMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQ 3403
Db 3324 HSLEAQDIMVKMESCMPNLETILAEVDQFVESDKTYNDAPHIIDVILPLLCAYLPFWWSQ 3383
Qy 3404 GPDNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSE 3463
Db 3384 GPDNVSPTSGNHVTMVTADHMNPLLRNVLKMIKKNIGNDNAPWMTRIAAYTQQIIINTSE 3443
Qy 3464 ELLRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSF 3523
Db 3444 ELLKDPFLPLAERVKKRTENMLHKEDSMRGFIKSATDDTSQVETQLQEDWNLLVRDIYSF 3503
Qy 3524 YPLLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMV 3583
Db 3504 YPLLIKYVDLQRNHWLKDNIPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMA 3563
Qy 3584 LIMPTATRRVTAVTDGTPQGGG--KKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNL 3641
Db 3564 LIMPTATRR-SAISEGAPAVGGKVKKKKKNRDKKRDKDKEVQASLMVACLKRLLPVGLNL 3622
Qy 3642 FAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSK 3701
Db 3623 FAGREQELVQHCKDRYLKKMPEYDVIEFARNQLTLPDKLDPSDEMSWQHYLYSKLG-KTE 3681
Qy 3702 SNITVETAENKAKI---------IDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVS 3752
Db 3682 EPVD-EQALEKANVNSNEKGKDKTQETVDRIVAMAKVLFGLHMIDHPQQQSKNVYRSVVS 3740
Qy 3753 IQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAEL 3812
Db 3741 IQRKRAVIACFRQTSLHSLPRHRACNIFARSYYEQWLQEENVGQEVMVEDLTQTFEDSEK 3800
Qy 3813 KKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGG 3872
Db 3801 SKKEGEETDSKPDPLTQLVTTFCRGAMTERSGALQEDLLYMSYAQIAAKSTGKEEEEGGD 3860
Qy 3873 EEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMV 3932
Db 3861 EE---GGEGGEEGEG-TSIHEQEMEKQKLLFHQARLSNRGVAEMVLLHISASKGIPSEMV 3916
Qy 3933 MKTLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAE 3992
Db 3917 MTTLNLGIAILRGGNIDIQMGMLNHLKEKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAE 3976

```
Qy       3993 GLGVGLEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTV 4052
Db       3977 GLGVGSEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLEWQNYLRTQAGNTTTVNVVICTV 4036

Qy       4053 DYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQAL 4112
Db       4037 DYLLRLQESIMDFYWHYSSKEIIDPAGKANFFKAIEVASQVFNTLTEVIQGPCTLNQQAL 4096

Qy       4113 AHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTI 4172
Db       4097 AHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTI 4156

Qy       4173 GKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQ 4232
Db       4157 GKQMVDTLVESASNVELILKYFDMFLKLADLIESPSFHEVDMKNEGWVTPKDFREKMEQS 4216

Qy       4233 KSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRL 4292
Db       4217 KNYTPEEMDFLLACCERNHEGKIDYRAFVEHFHEPSKEIGFNLAVLLTNLSEHMPNEPRL 4276

Qy       4293 ARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYS 4352
Db       4277 ARFLETAGSVLNYFEPFLGRIEILGSSKRIERVYFEIKDSNIEQWEKPQIRESKRAFFYS 4336

Qy       4353 IVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASY-MYMGDDDDER 4411
Db       4337 IVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRDTAYSSYMSEEEEER 4394

Qy       4412 AGKDPFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLG 4471
Db       4395 AARDPIRRTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIVGFFKIIFYIFYYTG 4454

Qy       4472 YGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADD 4531
Db       4455 YAHFCVVRYIFGILLNLMRGPAPEQEEEPVVEEETFG-----------RALPPLPLEEP 4502

Qy       4532 TGQMQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEE------- 4584
Db       4503 PGTVQ--AFGLDINKEENGMYKVVVHESPANSSMEEGGES--SPEDGAAASGELVEGEPH 4558

Qy       4585 QRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQGPAPS-ALSQVDLSQ 4643
Db       4559 QEPISIVDLLGGEAAKKAAQERQEAQKAQEAAMASIEAEAKKSSSAPQETPAVHQIDFSQ 4618

Qy       4644 YTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGS 4703
Db       4619 YTHRAVSFLARNFYNLKYVALVLAFSINFMLLFYKVTSFT-EEADSSAEEELILGSGSGG 4677

Qy       4704 GA---GS---GSGDGSGESGE-DDDALEVVHIDEDFFYMEHVIKMAAVLHSIVSLAILIG 4756
Db       4678 GADITGSGFGGSGDGGSGDGEMEDEIPELVHVDEDFFYMEHVLRIAACLHSLVSLAMLIA 4737

Qy       4757 YYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFV 4816
Db       4738 YYHLKVPLAIFKREKEIARRLEFEGLFIAEQPEDDDFKSHWDKLVISAKSFPVNYWDKFV 4797

Qy       4817 KKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTIT 4876
Db       4798 KKKVRQKYSETYDFDSISNLLGMEKSTFAAQESE-ETGIFKYIMNIDWRYQVWKAGVTFT 4856

Qy       4877 DNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLT 4936
Db       4857 DNAFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLT 4916

Qy       4937 IIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDG 4996
Db       4917 IIVYIYTVIAFNFFRKFYIQEEDEEVDKKCHDMLTCFVFHLYKGVRAGGGIGDEIGDPDG 4976

Qy       4997 DDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKD 5056
Db       4977 DDYEVYRIIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKDNMESNCFICGMGKD 5036

Qy       5057 YFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGD 5116
Db       5037 FFDIVPHGFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWNMYQQRSWDFFPVGD 5096

Qy       5117 CFRKQYED 5124
Db       5097 CFRKQYED 5104
```

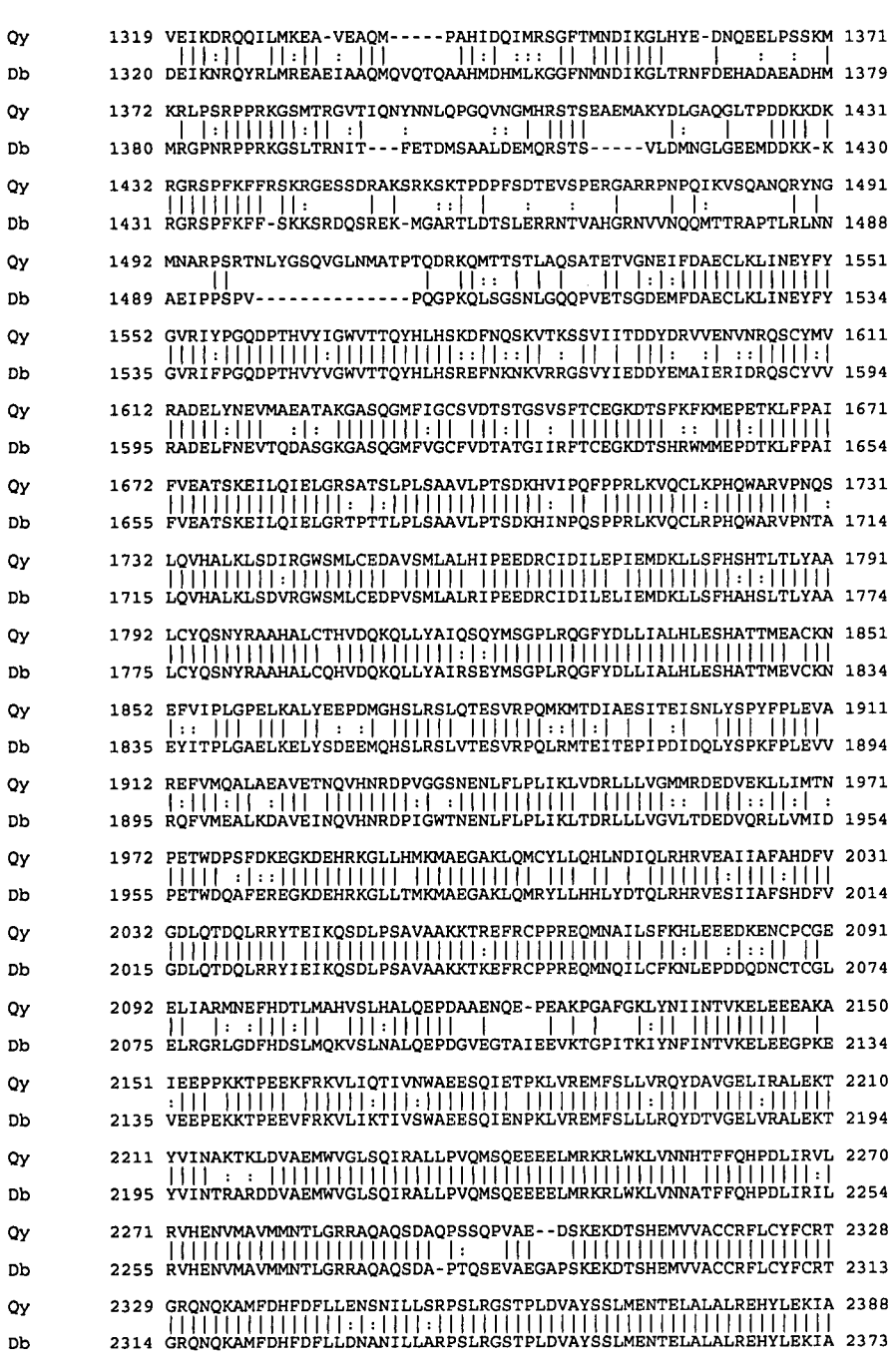
RESULT 9
US-10-668-767-120
; Sequence 120, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 5127
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: gi 17352465
US-10-668-767-120

Query Match 79.7%; Score 21360; DB 4; Length 5127;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 4090; Conservative 448; Mismatches 522; Indels 122; Gaps 41;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
```


Db 420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV----------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1894
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1895 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1954
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1955 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2014
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2015 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2074
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2075 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2134
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2135 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2194
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2195 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2254
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2255 NATFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2313
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2314 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2373
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2374 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2433
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2434 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2492
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2493 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILR 2552
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2553 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2612

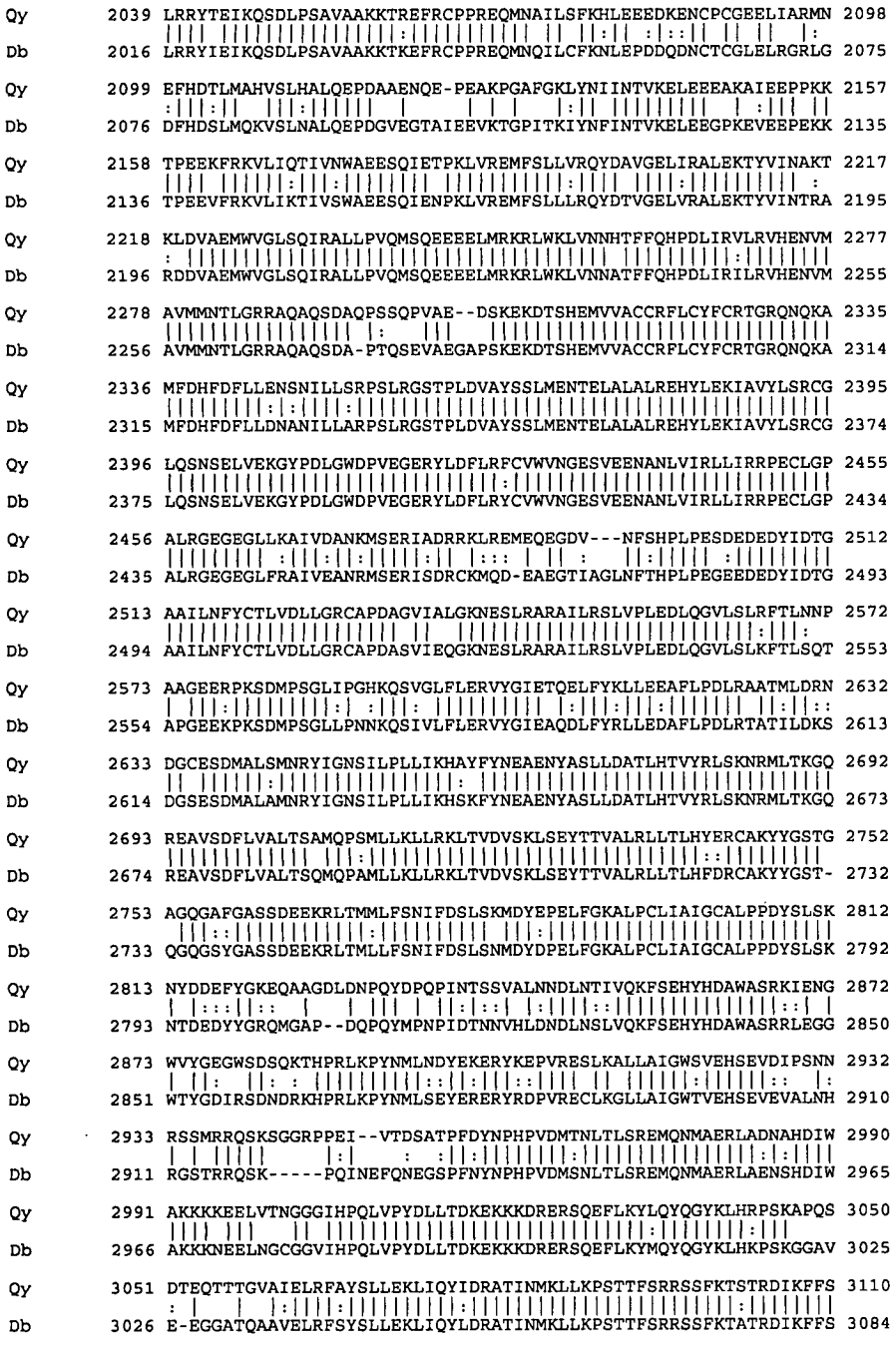
```
Db       4738 ACLHSLVSLAMLIAYYHLKVPLAIFKREKEIARRLEFEGLFIAEQPEDDDFKSHWDKLVI 4797

Qy       4803 SAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINI 4862
             |||||||||||||||||| |||||||||||||:|||||::|:||| |   |:  ||:||
Db       4798 SAKSFPVNYWDKFVKKKVRQKYSETYDFDSISNLLGMEKSTFAAQESE-ETGIFKYIMNI 4856

Qy       4863 DWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVT 4922
             |||||||||||| |||:|||||||||||||||||||||||||||||||||||||||||||||
Db       4857 DWRYQVWKAGVTFTDNAFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVT 4916

Qy       4923 HNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKGVR 4982
             ||||||||||||||||||||||||||||||||:||||:||:: ||||||||||:||||||
Db       4917 HNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYIQEEDEEVDKKCHDMLTCFVFHLYKGVR 4976

Qy       4983 AGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKE 5042
             ||||||||:  ||||| |||||||||:||||:|:|||||:||||||||||||||||||||:
Db       4977 AGGGIGDEIGDPDGDDYEVYRIIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKD 5036

Qy       5043 DMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWN 5102
              :|||||||||: ||:|| ||||||||||:||||||||||||||||||||||||||||||
Db       5037 NMESNCFICGMGKDFFDIVPHGFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWN 5096

Qy       5103 MYTQRCWDFFPVGDCFRKQYED 5124
              || || ||||||||||||||||
Db       5097 MYQQRSWDFFPVGDCFRKQYED 5118


RESULT 10
US-10-668-767-10
; Sequence 10, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 5109
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-668-767-10

  Query Match             79.6%;  Score 21326;  DB 4;  Length 5109;
  Best Local Similarity   79.0%;  Pred. No. 0;
  Matches 4081;  Conservative  450;  Mismatches  527;  Indels  108;  Gaps   40;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||| |||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:|||||||||:|||||||||||||| || ||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDGLIPVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||| ::

Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||||||||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||| ||||||||||:|||||||||||:|| |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:||  ||| ||||||||||||:||::|||||||:|||||||||||||||
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:||||||||||:|:|||||||| ||||||:||||::|| ||||||||||||||||||
Db        480 EGVLNLILEAIDKVNIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||:|| ||:|||||||||||||||||||||||||:|||||||||
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVVISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| ||||:|:|||||||:|
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||:|||||||:|||||||:|||||||||||:||
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:|||||  |     |||:|||||||| |:||:|||| | ||||:| ||| :|||:
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||:|||||||:|
Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::|||||| ||||  :|||: |:||::|||||||||||:|||||| :|:
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:| |:|||||  ||:|| |||||| ||||||||||::|||||::|||||||| ||||||
Db        900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||| ||||||||||||||::|||||||||||||||||||||||||||||||: ||
Db        960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:|||||||||||||||||||:|||||||  |||| || : | | ||
Db       1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||| |:||||:|||||||:||:|||||||| ||  || ||| :: ||||||:|  |::
Db       1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
              :|: | || ::  |||:| |:|: ::|||||||||||||||||||||  :|  ||||
Db       1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
              |||||||||||| ||||::||:|||||||||||||||||:| ||||||||||||:||
Db       1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
              | |||||||| |:|||| |||||||||||||||||||||||| |  ||| | ||||||
Db       1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
```


Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1715 LQVHALKLSDVRGWSMLCEDPVSMLALRIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1894
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1895 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1954
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1955 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMRYLLHHLYDTQLRHRVESIIAFSHDFV 2014
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2015 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2074
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
Db 2075 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2134
Qy 2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db 2135 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2194
Qy 2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db 2195 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2254
Qy 2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db 2255 RVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2313
Qy 2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db 2314 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2373
Qy 2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db 2374 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYPDFLRYCVWVNGESVEENANLVIRLLIR 2433
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db 2434 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2492
Qy 2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db 2493 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSL 2552
Qy 2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db 2553 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2612
Qy 2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
Db 2613 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2672
Qy 2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db 2673 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2732
Qy 2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db 2733 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2791
Qy 2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db 2792 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2849
Qy 2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db 2850 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2909
Qy 2926 VDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADN 2985
Db 2910 VEVPLNHRGSTRRQSK-----PQI--NEGSPFNYNPHPVDMSNLTLSREMQNMAERLAEN 2962
Qy 2986 AHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPS 3045
Db 2963 SHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQEFLKYMQYQGYKLHKPS 3022
Qy 3046 KAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRD 3105
Db 3023 KGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKPSTTFSRRSSFKTATRD 3081
Qy 3106 IKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLA 3165
Db 3082 IKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMVASIFCKLAALLRNRLS 3141
Qy 3166 AFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKY 3225
Db 3142 AFGPDVRITVRCLQVLVKGIDARTLTKNCPEFIRTSMLTFFNQTSDDLGNTILNLQDGKY 3201
Qy 3226 AHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYAL 3285
Db 3202 SHLRGTHLKTSTSLGYVNQVVLPVLTAMFDHLAACDYGSDLLLDEIQVASYKILAALYHL 3261
Qy 3286 GTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHS 3345
Db 3262 GTDGTLTHDRKYLKTEIERHRPALGSCLGAYSSCFPVAFLEPHLNKHNQYSLLNRIADHS 3321
Qy 3346 LEAQDIMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGP 3405
Db 3322 LEAQDIMVKMESCMPNLETILAEVDQFVESDKTYNDAPHIIDVILPLLCAYLPFWWSQGP 3381
Qy 3406 DNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEEL 3465
Db 3382 DNVSPTSGNHVTMVTADHMNPLLRNVLKMIKKNIGNDNAPWMTRIAAYTQQIIINTSEEL 3441
Qy 3466 LRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYP 3525

```
Db       3442 LKDPFLPLAERVKKRTENMLHKEDSMRGFIKSATDDTSQVETQLQEDWNLLVRDIYSFYP 3501

Qy       3526 LLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLI 3585

Db       3502 LLIKYVDLQRNHWLKDNIPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMALI 3561

Qy       3586 MPTATRRVTAVTDGTPQGGG--KKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFA 3643

Db       3562 MPTATRR-SAISEGAPAVGGKVKKKKKNRDKKRDKDKEVQASLMVACLKRLLPVGLNLFA 3620

Qy       3644 GREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSN 3703

Db       3621 GREQELVQHCKDRYLKKMPEYDVIEFARNQLTLPDKLDPSDEMSWQHYLYSKLG-KTEEP 3679

Qy       3704 ITVETAENKAKI---------IDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQ 3754

Db       3680 VD-EQALEKANVNSNEKGKDKTQETVDRIVAMAKVLFGLHMIDHPQQQSKNVYRSVVSIQ 3738

Qy       3755 RKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKK 3814

Db       3739 RKRAVIACFRQTSLHSLPRHRACNIFARSYYEQWLQEENVGQEVMVEDLTQTFEDSEKSK 3798

Qy       3815 SDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEE 3874

Db       3799 KEGEETDSKPDPLTQLVTTFCRGAMTERSGALQEDLLYMSYAQIAAKSTGKEEEEGGDEE 3858

Qy       3875 EEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMK 3934

Db       3859 ---GGEGGEEAEG-TSIHEQEMEKQKLLFHQARLSNRGVAEMVLLHVSASKGIPSEMVMT 3914

Qy       3935 TLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGL 3994

Db       3915 TLNLGIAILRGGNIDIQMGMLNHLKEKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGL 3974

Qy       3995 GVGLEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDY 4054

Db       3975 GVGSEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLEWQNYLRTQAGNTTTVNVVICTVDY 4034

Qy       4055 LLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAH 4114

Db       4035 LLRLQESIMDFYWHYSSKEIIDPAGKANFFKAIEVASQVFNTLTEVIQGPCTLNQQALAH 4094

Qy       4115 SRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGK 4174

Db       4095 SRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGK 4154

Qy       4175 QMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKS 4234

Db       4155 QMVDTLVESASNVELILKYFDMFLKLADLIESPSFHEVDMKNEGWVTPKDFREKMEQSKN 4214

Qy       4235 YTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLAR 4294

Db       4215 YTPEEMDFLLACCERNHEGKIDYRAFVEHFHEPSKEIGFNLAVLLTNLSEHMPNEPRLAR 4274

Qy       4295 FLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIV 4354

Db       4275 FLETAGSVLNYFEPFLGRIEILGSSKRIERVYFEIKDSNIEQWEKPQIRESKRAFFYSIV 4334

Qy       4355 TEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASY-MYMGDDDDERAG 4413

Db       4335 TEGGDKEKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRDTAYSSYMSEEEEERAA 4392

Qy       4414 KDPFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYG 4473

Db       4393 RDPIRRTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIVGFFKIIFYIFYYTGYA 4452

Qy       4474 VLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTG 4533

Db       4453 HFCVVRYIFGILLNLMRGPAPEQEEEPVVEEETFG-----------RALPPLSLEEPPG 4500

Qy       4534 QMQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEE-------QR 4586

Db       4501 TVQ--AFGLDINKEENGMYKVVVHESPANSSMEEGGES--SPEDGAAASGELVEGEPHQG 4556

Qy       4587 PPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQGPAPS-ALSQVDLSQYT 4645

Db       4557 PISIVDLLGGEAAKKAAQERQEAQKAQEAAMASIEAEAKKSSSAPQETPAVHQIDFSQYT 4616

Qy       4646 RRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGA 4705

Db       4617 HRAVSFLARNFYNLKYVALVLAFSINFMLLFYKVTSFT-EEADSSAEEELILGSGPGGGA 4675

Qy       4706 ---GS---GSGDGSGESGE-DDDALEVVHIDEDFFYMEHVIKMAAVLHSIVSLAILIGYY 4758

Db       4676 DITGSGFGGSGDGGSGDGEMEDEIPELVHVDEDFFYMEHVLRIAACLHSLVSLAMLIAYY 4735

Qy       4759 HLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFVKK 4818

Db       4736 HLKVPLAIFKREKEIARRLEFEGLFIAEQPEDDDFKSHWDKLVISAKSFPVNYWDKFVKK 4795

Qy       4819 KVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTITDN 4878

Db       4796 KVRQKYSETYDFDSISNLLGMEKSTFAAQESE-ETGIFKYIMNIDWRYQVWKAGVTFTDN 4854

Qy       4879 SFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTII 4938

Db       4855 AFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTII 4914

Qy       4939 VYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDD 4998

Db       4915 VYIYTVIAFNFFRKFYIQEEDEEVDKKCHDMLTCFVFHLYKGARAGGGIGDEIGDPDGDD 4974

Qy       4999 SEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYF 5058

Db       4975 YEVYRIIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKDNMESNCFICGMGKDFF 5034

Qy       5059 DKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGDCF 5118

Db       5035 DIVPHGFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWNMYQQRSWDFFPVGDCF 5094

Qy       5119 RKQYED 5124

Db       5095 RKQYED 5100
```

RESULT 11
US-11-097-143-22563
; Sequence 22563, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22563
;   LENGTH: 5107
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-22563

  Query Match             79.4%;  Score 21270.5;  DB 6;  Length 5107;
  Best Local Similarity   78.9%;  Pred. No. 0;
  Matches 4070;  Conservative  448;  Mismatches  522;  Indels  121;  Gaps   40;

Qy         22 MVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDLSQCVFVIEQALSVRALQELVT 81
Db          1 MVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDLSQCVFVIEQALSVRALQELVT 60

Qy         82 AAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSSQDKLAFDVGLQQHSQGEA 141
Db         61 AAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLSTSSSNDKLSFDVGLQEHSQGEA 120

Qy        142 CWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPY 201
Db        121 CWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTKENEQSIVNASFHVTHWSVQPY 180

Qy        202 GTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWR 261
Db        181 GTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREAGQNIVIYEGGVVMAQARSLWR 240

Qy        262 LELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKD 321
Db        241 LELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELILVKKEEASIATTTFCLRQEKD 300

Qy        322 DQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILH 381
Db        301 DEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSYKSYETKKKGVGKVEEKQAILH 360

Qy        382 EEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEM 441
Db        361 EEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITALETLQSNRRHSIFFQKVNLNEM 420

Qy        442 VMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQG 501
Db        421 VMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQEEGVLNLILEAIDKINIITSQG 480

Qy        502 FLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGE 561
Db        481 FLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASSE 540

Qy        562 GTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRS 621
Db        541 GSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRS 600

Qy        622 SQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTH 681
Db        601 SQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDGSSMYQKWYFEVTMDHIEQTTH 660

Qy        682 MMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEE 741
Db        661 MMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGFDGAFLWTGGRKTLVVDALPEE 720

Qy        742 PYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGG 801
Db        721 PFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLDGMFFPVMSCSSKLSCRFLFGG 780

Qy        802 EHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSKRALAGPPLVQDDTAFVPTPVD 861
Db        781 DHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAKNVLAGPWLIEDDTAFVPKPVD 840

Qy        862 TLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAE 921
Db        841 TTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEHRDDYHRIHPCLTHFEKLPAAE 900

Qy        922 KRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLT 981
Db        901 KRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNEIFMQGNGYKPAPLDLSAVTLT 960

Qy        982 PKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDT 1041
Db        961 PKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHRSPHLVPYAKVDEAIKKANRDT 1020

Qy       1042 ASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEI 1101
Db       1021 ASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFRTYRVERNYAVTSGKWYFEFEV 1080

Qy       1102 LTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFL 1161
Db       1081 LTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMHAGSIEHFGVRYEAGDVIGCFI 1140

Qy       1162 DLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPACTLGVGQKARLTYGQDVNTLK 1219
Db       1141 DVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPACTLGVGQKARLIYGQDVDSLK 1200

Qy       1220 YFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLK 1279
Db       1201 FFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEMPDCRIDVTRIPGGADTPPHLK 1260

Qy       1280 ISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEA-VEAQM- 1337
Db       1261 ISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRWDEIKNRQYRLMREAEIAAQMQ 1320

Qy       1338 ----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKMKRLPSRPPRKGSMTRGVTIQN 1392
Db       1321 VQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHMMRGPNRPPRKGSLTRNIT--- 1377

Qy       1393 YNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAK 1452
Db       1378 FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-KRGRSPFKFF-SKKSRDQSREK 1430

Qy       1453 SRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMAT 1512
Db       1431 -MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNNAEIPPSPV------------- 1476

Qy       1513 PTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQ 1572
Db       1477 -PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFYGVRIFPGQDPTHVYVGWVTTQ 1535

Qy       1573 YHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQG 1632
Db       1536 YHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVVRADELFNEVTQDASGKGASQG 1595

Qy       1633 MFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSL 1692
Db       1596 MFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAIFVEATSKEILQIELGRTPTTL 1655

Qy       1693 PLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDA 1752
Db       1656 PLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTALQVHALKLSDVRGWSMLCEDP 1715

Qy       1753 VSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQ 1812
Db       1716 VSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAALCYQSNYRAAHALCQHVDQKQ 1775

Qy       1813 LLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPELKALYEEPDMGH 1872
Db       1776 LLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKNEYITPLGAELKELYSDEEMQH 1835

Qy       1873 SLRSLQTESVRPQMKMTDI--------------AESITEISNLYSPYFPLEVAREFVMQA 1918
Db       1836 SLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPDIDQLYSPKFPLEVVRQFVMEA 1895

Qy       1919 LAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPS 1978
Db       1896 LKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMIDPETWDQA 1955

Qy       1979 FDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQ 2038
Db       1956 FEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFVGDLQTDQ 2015
```

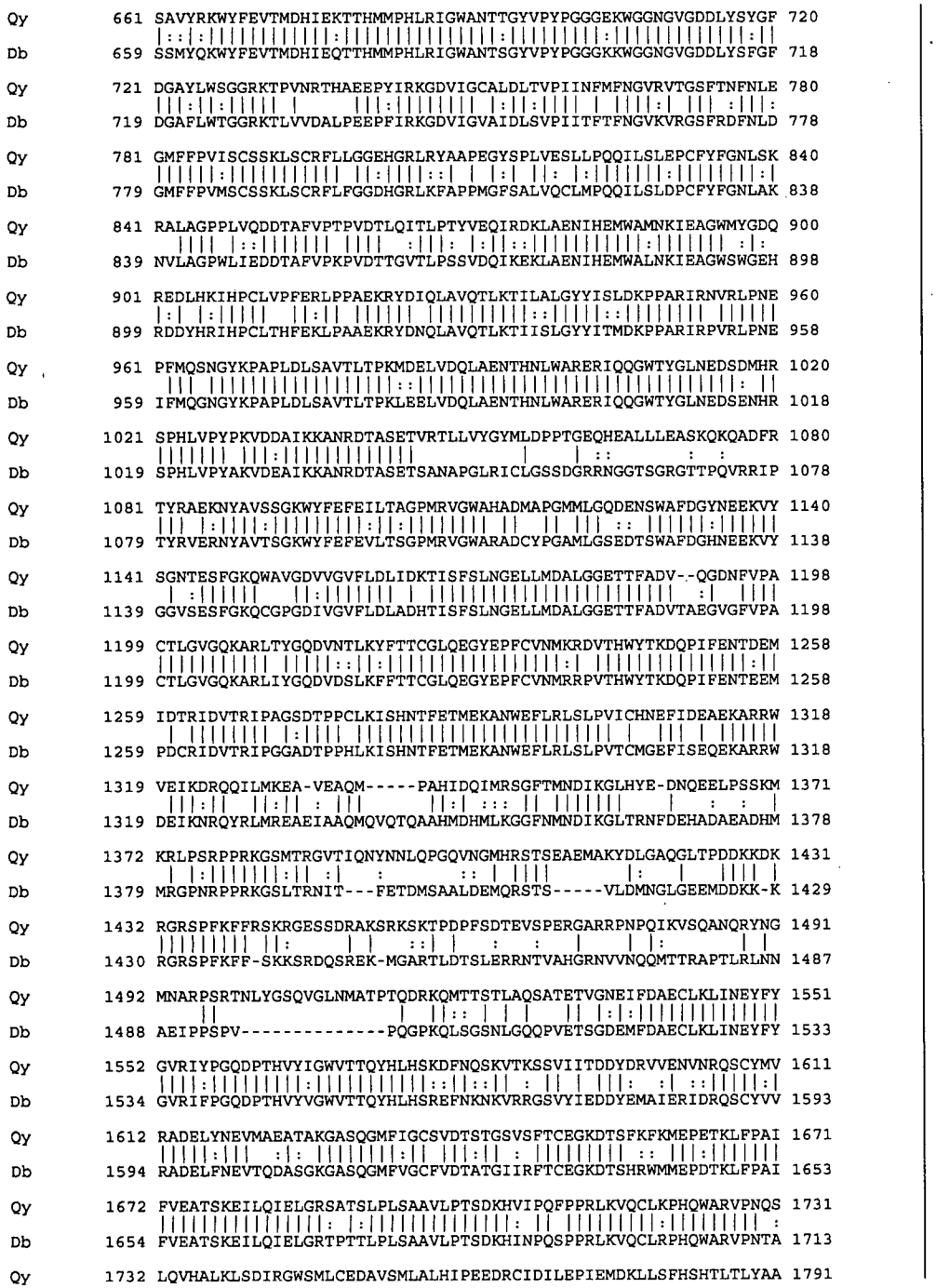

Qy 2039 LRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098
Db 2016 LRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGLELRGRLG 2075
Qy 2099 EFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKK 2157
Db 2076 DFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKEVEEPEKK 2135
Qy 2158 TPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKT 2217
Db 2136 TPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKTYVINTRA 2195
Qy 2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277
Db 2196 RDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRILRVHENVM 2255
Qy 2278 AVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2335
Db 2256 AVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2314
Qy 2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395
Db 2315 MFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2374
Qy 2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
Db 2375 LQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIRRPECLGP 2434
Qy 2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDEDEDYIDTG 2512
Db 2435 ALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEEDEDYIDTG 2493
Qy 2513 AAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNP 2572
Db 2494 AAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSLKFTLSQT 2553
Qy 2573 AAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRN 2632
Db 2554 APGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRTATILDKS 2613
Qy 2633 DGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2692
Db 2614 DGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2673
Qy 2693 REAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTG 2752
Db 2674 REAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCAKYYGST- 2732
Qy 2753 AGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSK 2812
Db 2733 QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALPPDYSLSK 2792
Qy 2813 NYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENG 2872
Db 2793 NTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWASRRLEGG 2850
Qy 2873 WVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNN 2932
Db 2851 WTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSEVEVALNH 2910
Qy 2933 RSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIW 2990
Db 2911 RGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLAENSHDIW 2965
Qy 2991 AKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQS 3050
Db 2966 AKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQEFLKYMQYQGYKLHKPSKGGAV 3025
Qy 3051 DTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTSTRDIKFFS 3110
Db 3026 E-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKPSTTFSRRSSFKTATRDIKFFS 3084
Qy 3111 KAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPD 3170
Db 3085 KVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMVASIFCKLAALLRNRLSAFGPD 3144
Qy 3171 VRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRG 3230
Db 3145 VRITVRCLQVLVKGIDARTLTKNCPEFIRTSMLTFFNQTSDDLGNTILNLQDGKYSHLRG 3204
Qy 3231 THLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDAS 3290
Db 3205 THLKTSTSLGYVNQVVLPVLTAMFDHLAACDYGSDLLLDEIQVASYKILAALYHLGTDGT 3264
Qy 3291 LTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQD 3350
Db 3265 LTHDRKYLKTEIERHRPALGSCLGAYSSCFPVAFLEPHLNKHNQYSLLNRIADHSLEAQD 3324
Qy 3351 IMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTP 3410
Db 3325 IMVKMESCMPNLETILAEVDQFVESDKTYNDAPHIIDVILPLLCAYLPFWWSQGPDNVSP 3384
Qy 3411 TGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSF 3470
Db 3385 TSGNHVTMVTADHMNPLLRNVLKMIKKNIGNDNAPWMTRIAAYTQQIIINTSEELLKDPF 3444
Qy 3471 LPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQIQEDWQLLVRDIYSFYPLLIKY 3530
Db 3445 LPLAERVKKRTENMLHKEDSMRGFIKSATDDTSQVETQLQEDWNLLVRDIYSFYPLLIKY 3504
Qy 3531 VDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTAT 3590
Db 3505 VDLQRNHWLKDNIPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMALIMPTAT 3564
Qy 3591 RRVTAVTDGTPQGGG--KKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQE 3648
Db 3565 RR-SAISEGAPAVGGKVKKKKKNRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQE 3623
Qy 3649 LVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLGSKSKSNITVET 3708
Db 3624 LVQHCKDRYLKKMPEYDVIEFARNQLTLPDKLDPSDEMSWQHYLYSKLG-KTEEPVD-EQ 3681
Qy 3709 AENKAKI---------IDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAV 3759
Db 3682 ALEKANVNSNEKGKDKTQETVDRIVAMAKVLFGLHMIDHPQQQSKNVYRSVVSIQRKRAV 3741
Qy 3760 IACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEVMIEDLTQSFEDAELKKSDVVE 3819
Db 3742 IACFRQTSLHSLPRHRACNIFARSYYEQWLQEENVGQEVMVEDLTQTFEDSEKSKKEGEE 3801
Qy 3820 EGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEEEGGGEEEEGGG 3879
Db 3802 TDSKPDPLTQLVTTFCRGAMTERSGALQEDLLYMSYAQIAAKSTGKEEEEGGDEE---GG 3858
Qy 3880 EAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVLLHISASKGLPSEMVMKTLQLG 3939
Db 3859 EGGEEGEG-TSIHEQEMEKQKLLFHQARLSNRGVAEMVLLHISASKGIPSEMVMTTLNLG 3917
Qy 3940 ISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLE 3999
Db 3918 IAILRGGNIDIQMGMLNHLKEKKDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGSE 3977
Qy 4000 GAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTTVNVVICTVDYLLRLQ 4059
Db 3978 GAAGEKNMHDAEFTCALFRFIQLTCEGHNLEWQNYLRTQAGNTTTVNVVICTVDYLLRLQ 4037
Qy 4060 ESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWD 4119
Db 4038 ESIMDFYWHYSSKEIIDPAGKANFFKAIEVASQVFNTLTEVIQGPCTLNQQALAHSRLWD 4097
Qy 4120 AVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDT 4179
Db 4098 AVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGKQMVDT 4157
Qy 4180 LVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEE 4239

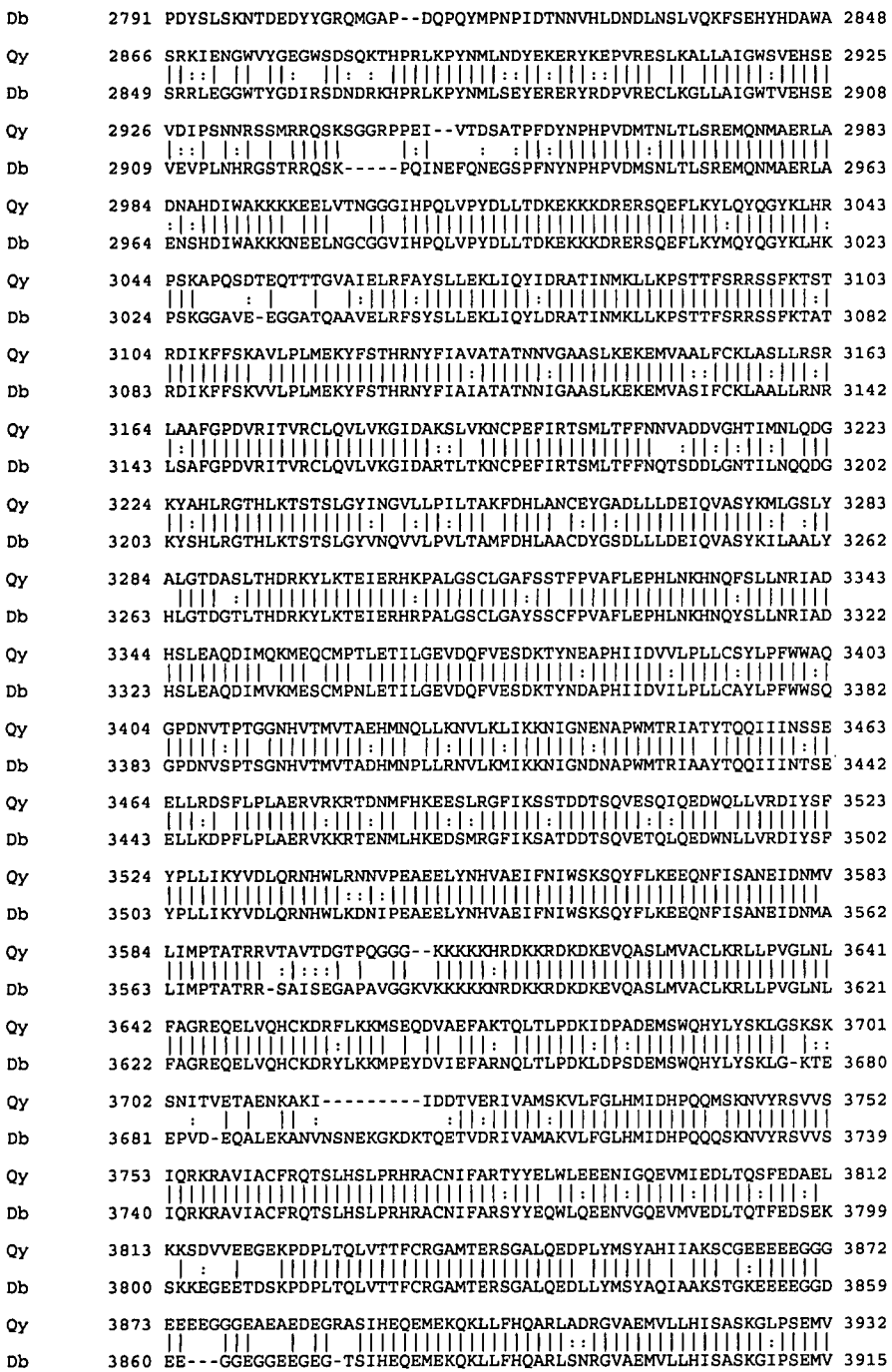
```
Db       4158 LVESASNVELILKYFDMFLKLADLIESPSFHEVDMKNEGWVTPKDFREKMEQSKNYTPEE 4217

Qy       4240 IEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETA 4299

Db       4218 MDFLLACCERNHEGKIDYRAFVEHFHEPSKEIGFNLAVLLTNLSEHMPNEPRLARFLETA 4277

Qy       4300 GSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSIVTEGGD 4359

Db       4278 GSVLNYFEPFLGRIEILGSSKRIERVYFEIKDSNIEQWEKPQIRESKRAFFYSIVTEGGD 4337

Qy       4360 KEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASY-MYMGDDDDERAGKDPFR 4418

Db       4338 KEKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRDTAYSSYMSEEEEERAARDPIR 4395

Qy       4419 RGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVV 4478

Db       4396 RTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIVGFFKIIFYIFYYTGYAHFCVV 4455

Qy       4479 RYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVS 4538

Db       4456 RYIFGILLNLMRGPAPEQEEEPVVEEETFG------------RALPPLPLEEPPGTVQ-- 4501

Qy       4539 AFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEE-------QRPPSLI 4591

Db       4502 AFGLDINKEENGMYKVVVHESPANSSMEEGGES--SPEDGAAASGELVEGEPHQEPISIV 4559

Qy       4592 DLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQGPAPS-ALSQVDLSQYTRRAVS 4650

Db       4560 DLLGGEAAKKAAQERQEAQKAQEAAMASIEAEAKKSSSAPQETPAVHQIDFSQYTHRAVS 4619

Qy       4651 FLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGSGA---GS 4707

Db       4620 FLARNFYNLKYVALVLAFSINFMLLFYKVTSFT-EEADSSAEEELILGSGSGGGADITGS 4678

Qy       4708 ---GSGDGSGESGE-DDDALEVVHIDEDFFYMEHVIKMAAVLHSIVSLAILIGYYHLKVP 4763

Db       4679 GFGGSGDGGSGDGEMEDEIPELVHVDEDFFYMEHVLRIAACLHSLVSLAMLIAYYHLKVP 4738

Qy       4764 LAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFVKKKVRAK 4823

Db       4739 LAIFKREKEIARRLEFEGLFIAEQPEDDDFKSHWDKLVISAKSFPVNYWDKFVKKKVRQK 4798

Qy       4824 YSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTITDNSFLYS 4883

Db       4799 YSETYDFDSISNLLGMEKSTFAAQESE-ETGIFKYIMNIDWRYQVWKAGVTFTDNAFLYS 4857

Qy       4884 LWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYT 4943

Db       4858 LWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIVYIYT 4917

Qy       4944 VIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEVYR 5003

Db       4918 VIAFNFFRKFYIQEEDEEVDKKCHDMLTCFVFHLYKGVRAGGGIGDEIGDPDGDDYEVYR 4977

Qy       5004 IIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPH 5063

Db       4978 IIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKDNMESNCFICGMGKDFFDIVPH 5037

Qy       5064 GFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGDCFRKQYE 5123

Db       5038 GFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWNMYQQRSWDFFPVGDCFRKQYE 5097

Qy       5124 D 5124

Db       5098 D 5098
```

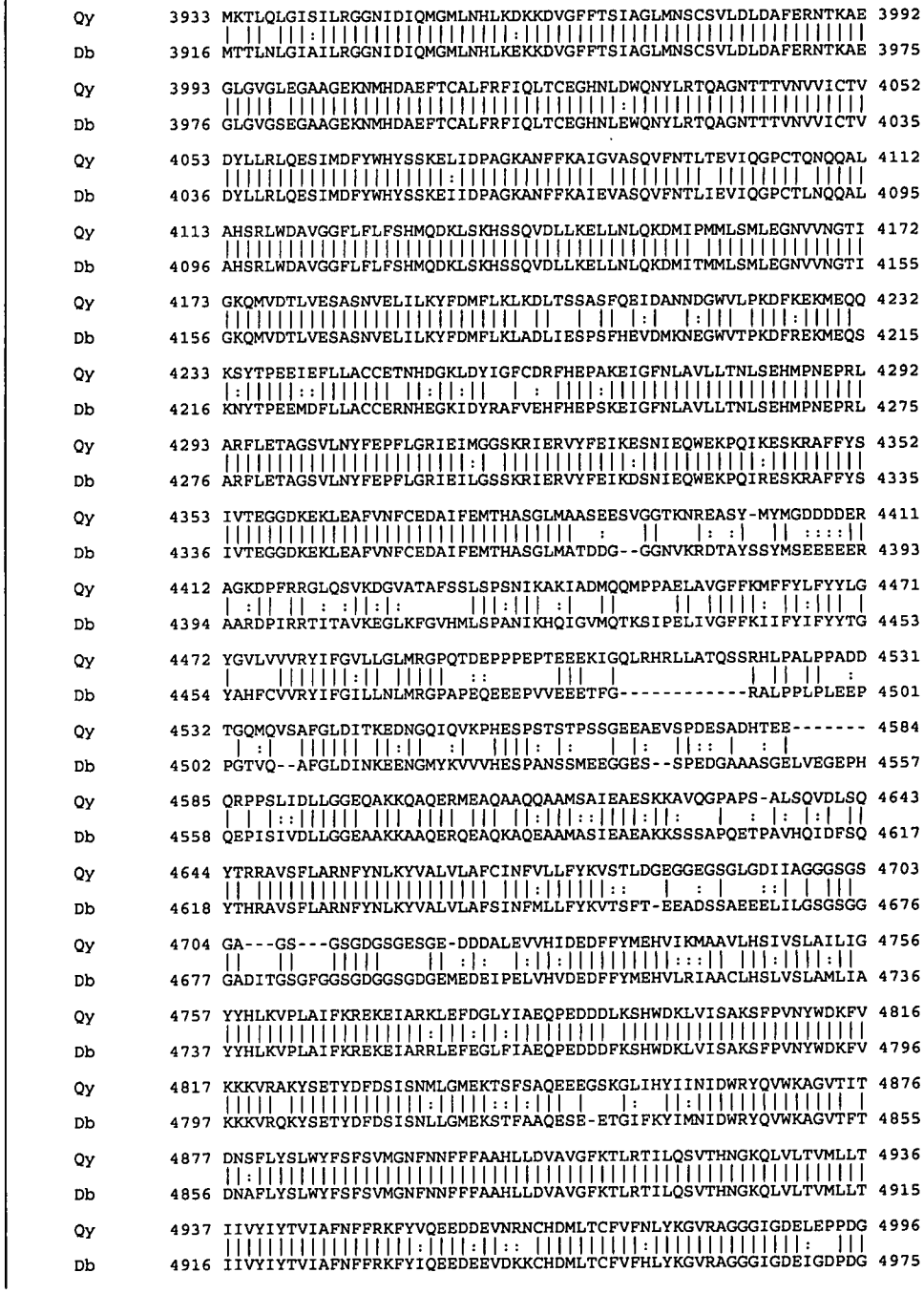
RESULT 12
US-10-668-767-125
; Sequence 125, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 5112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: gi 2160477
US-10-668-767-125

Query Match 79.2%; Score 21234.5; DB 4; Length 5112;
Best Local Similarity 78.8%; Pred. No. 0;
Matches 4072; Conservative 441; Mismatches 546; Indels 109; Gaps 41;

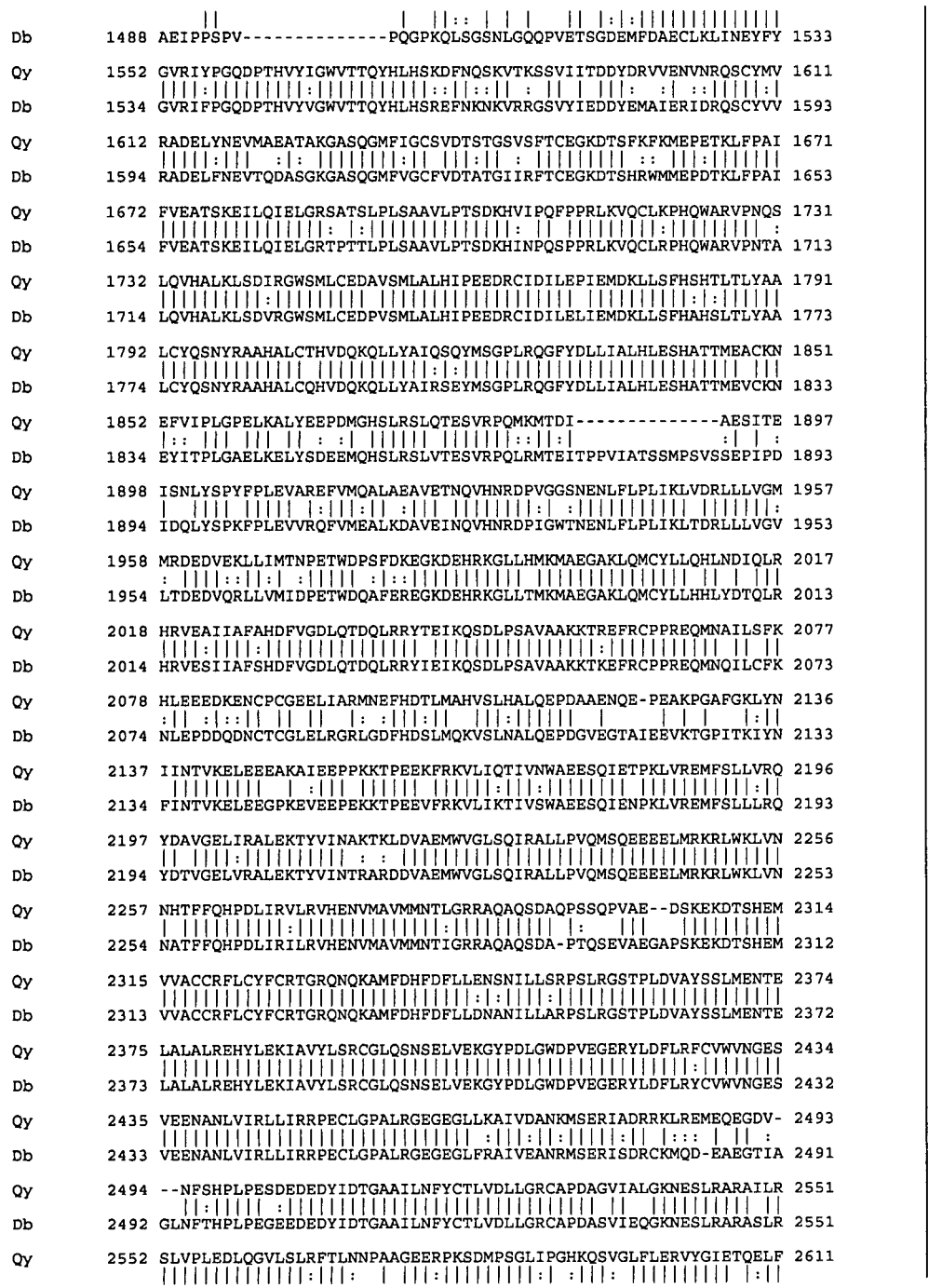
```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658
```

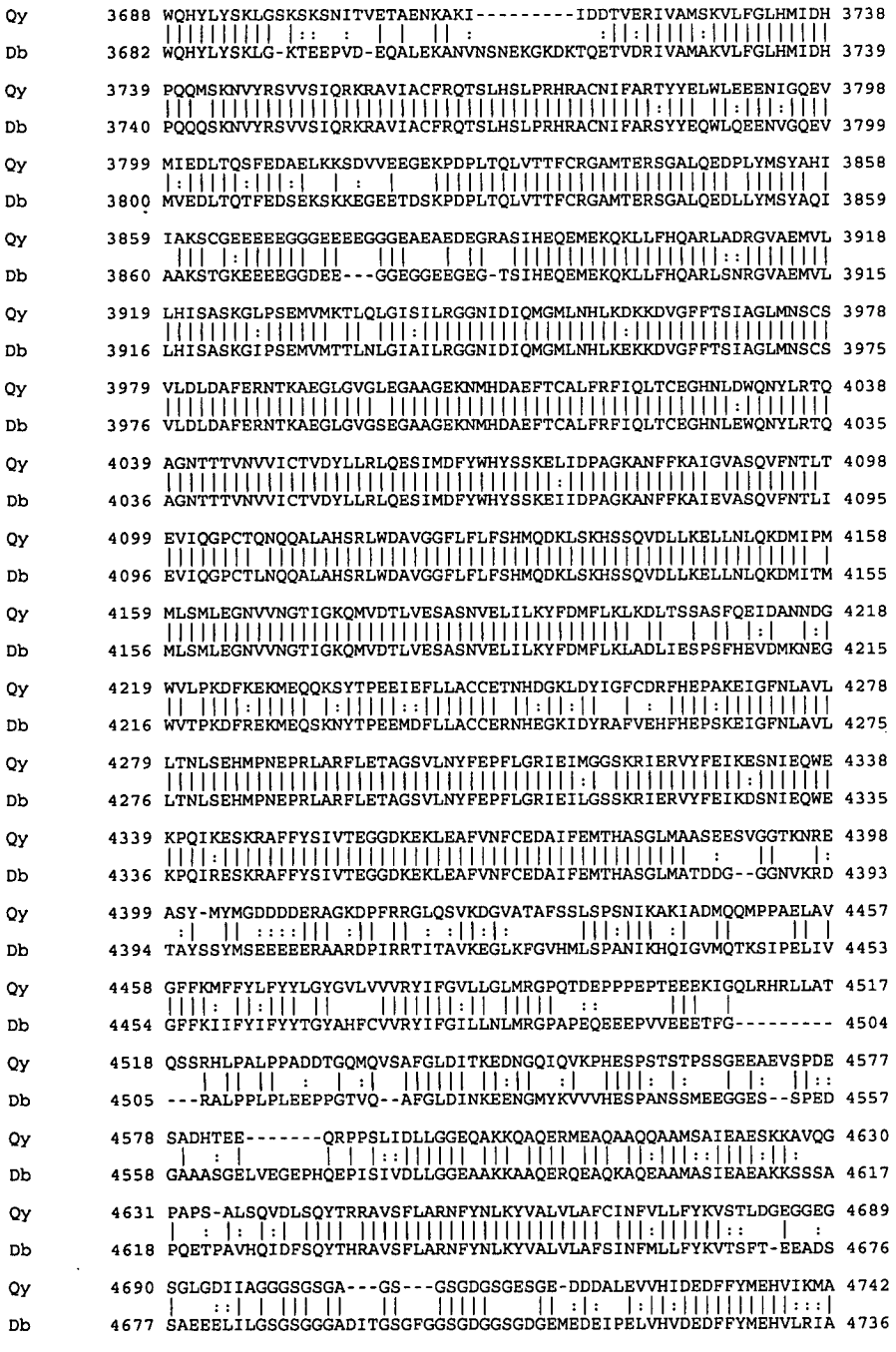


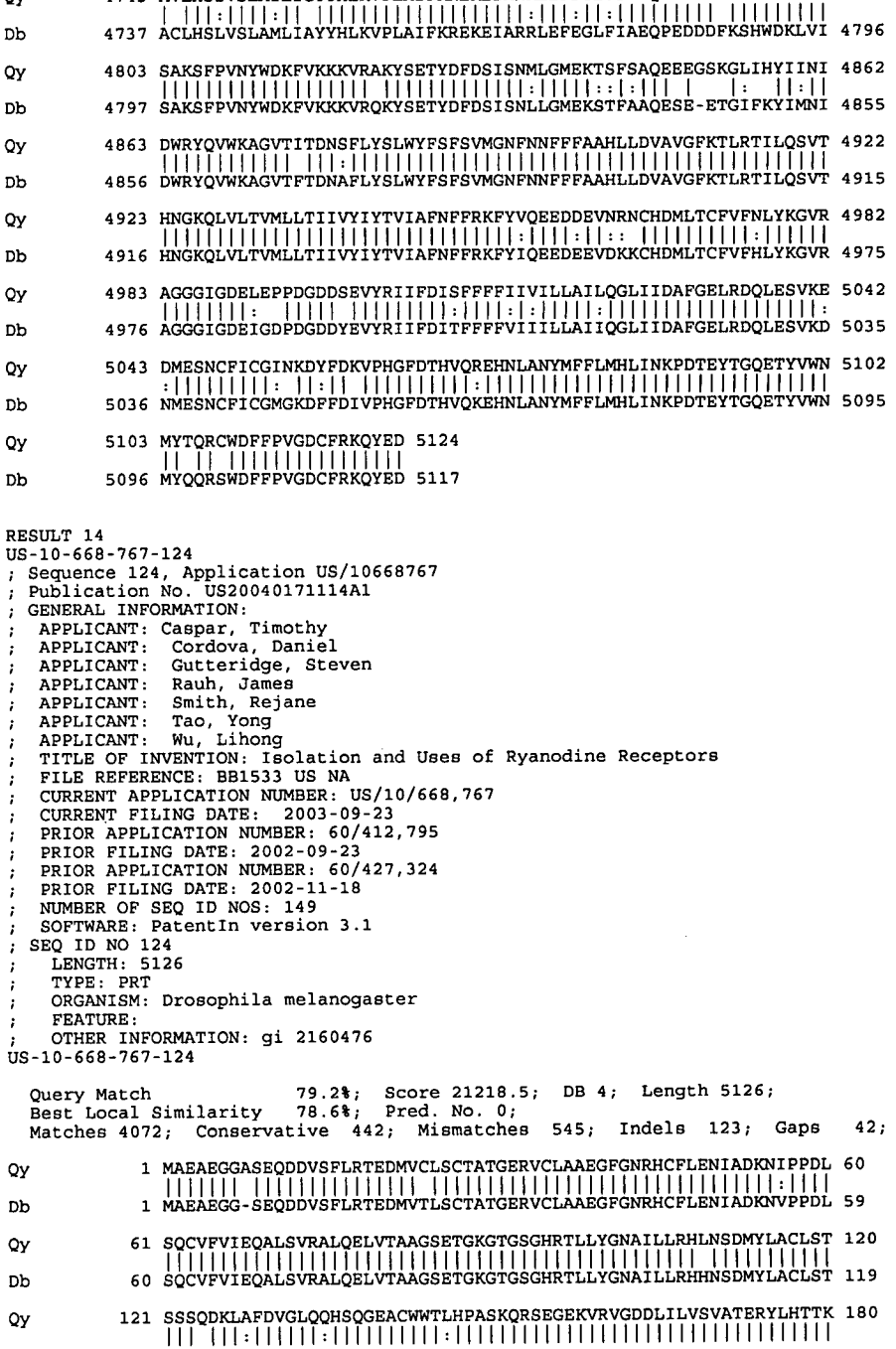




```
Qy       4997 DDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKD 5056
Db       4976 DDYEVYRIIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKDNMESNCFICGMGKD 5035

Qy       5057 YFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFPVGD 5116
Db       5036 FFDIVPHGFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWNMYQQRSWDFFPVGD 5095

Qy       5117 CFRKQYED 5124
Db       5096 CFRKQYED 5103


RESULT 13
US-10-668-767-56
; Sequence 56, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 5126
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-668-767-56

  Query Match             79.2%;  Score 21218.5;  DB 4;  Length 5126;
  Best Local Similarity   78.6%;  Pred. No. 0;
  Matches 4072;  Conservative  442;  Mismatches  545;  Indels  123;  Gaps   42;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db        659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        719 DGAFLWTGGRKTLVVDALPEEPPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db        779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db        839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db        899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db        959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db       1019 SPHLVPYAKVDEAIKKANRDTASETSANAPGLRICLGSSDGRRNGGTSGRGTTPQVRRIP 1078

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db       1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1138

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db       1139 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db       1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1258

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db       1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db       1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378

Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db       1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db       1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
```

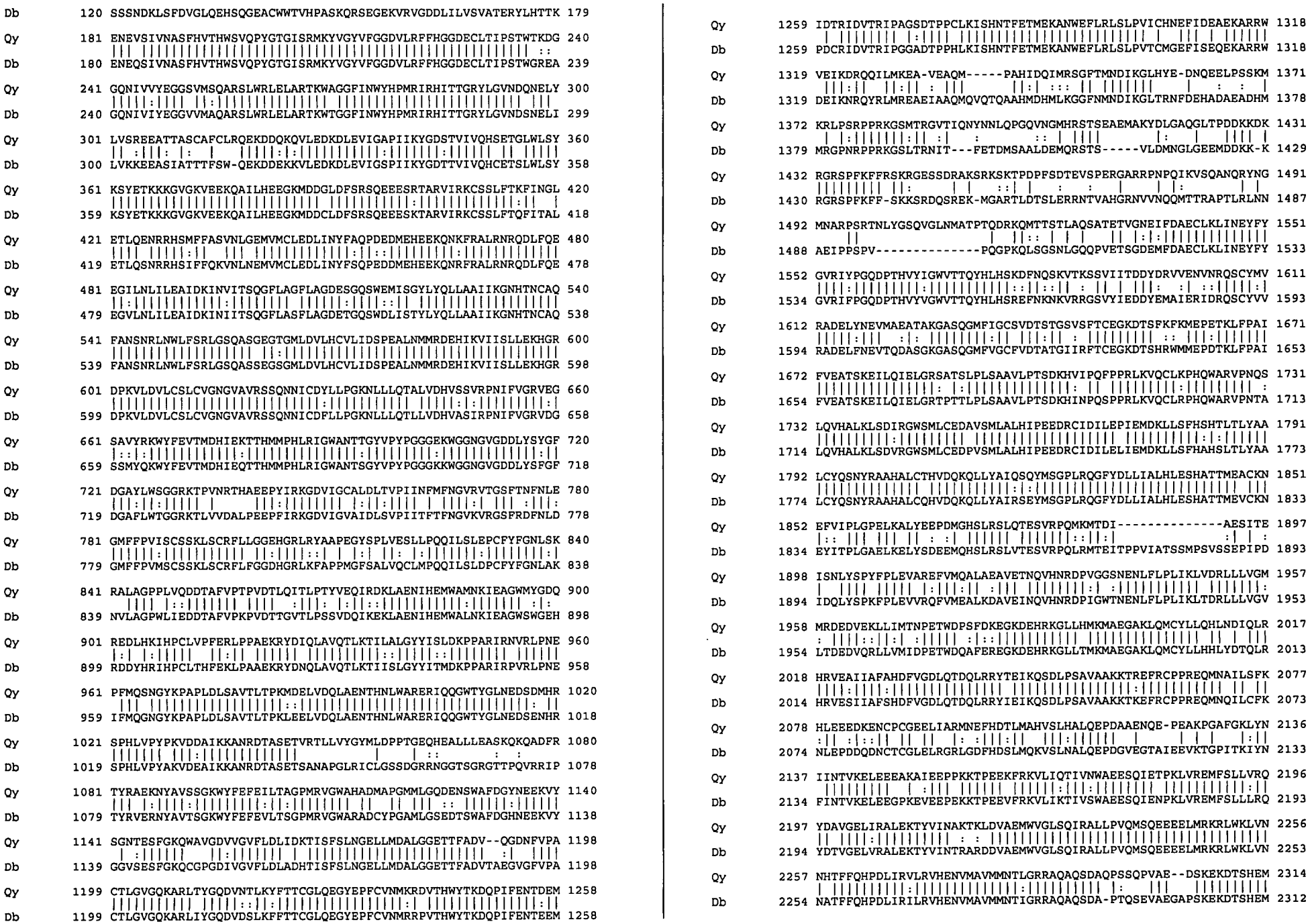

Db 1488 AEIPPSPV----------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1714 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1773
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1774 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1833
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1893
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1894 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1953
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1954 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2013
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2014 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2073
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2074 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2133
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2134 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2193
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2194 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2253
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2254 NATFFQHPDLIRILRVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2312
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2313 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2372
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2433 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2491
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2492 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLR 2551
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2552 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2611
Qy 2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db 2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671
Qy 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731
Qy 2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db 2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
Db 2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848
Qy 2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db 2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908
Qy 2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
Db 2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963
Qy 2970 TLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQE 3029
Db 2964 TLSREMQNMAERLAENSHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQE 3023
Qy 3030 FLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKP 3089
Db 3024 FLKYMQYQGYKLHKPSKGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKP 3082
Qy 3090 STTFSRRSSFKTSTRDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMV 3149
Db 3083 STTFSRRSSFKTATRDIKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMV 3142
Qy 3150 AALFCKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNV 3209
Db 3143 ASIFCKLAALLRNRLSAFGPDVRITVRCLQVLVKGIDARTLTKNCPEFIRTSMLTFFNQT 3202
Qy 3210 ADDVGHTIMNLQDGKYAHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLD 3269
Db 3203 SDDLGNTILNQQDGKYSHLRGTHLKTSTSLGYVNQVVLPVLTAMFDHLAACDYGSDLLLD 3262
Qy 3270 EIQVASYKMLGSLYALGTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHL 3329
Db 3263 EIQVASYKILAALYHLGTDGTLTHDRKYLKTEIERHRPALGSCLGAYSSCFPVAFLEPHL 3322
Qy 3330 NKHNQFSLLNRIADHSLEAQDIMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVV 3389
Db 3323 NKHNQYSLLNRIADHSLEAQDIMVKMESCMPNLETILGEVDQFVESDKTYNDAPHIIDVI 3382
Qy 3390 LPLLCSYLPFWWAQGPDNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTR 3449
Db 3383 LPLLCAYLPFWWSQGPDNVSPTSGNHVTMVTADHMNPLLRNVLKMIKKNIGNDNAPWMTR 3442
Qy 3450 IATYTQQIIINSSEELLRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQI 3509
Db 3443 IAAYTQQIIINTSEELLKDPFLPLAERVKKRTENMLHKEDSMRGFIKSATDDTSQVETQL 3502
Qy 3510 QEDWQLLVRDIYSFYPLLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKE 3569
Db 3503 QEDWNLLVRDIYSFYPLLIKYVDLQRNHWLKDNIPEAEELYNHVAEIFNIWSKSQYFLKE 3562
Qy 3570 EQNFISANEIDNMVLIMPTATRRVTAVTDGTPQGGG--KKKKKHRDKKRDKDKEVQASLM 3627
Db 3563 EQNFISANEIDNMALIMPTATRR-SAISEGAPAVGGKVKKKKKNRDKKRDKDKEVQASLM 3621
Qy 3628 VACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMS 3687
Db 3622 VACLKRLLPVGLNLFAGREQELVQHCKDRYLKKMPEYDVIEFARNQLTLPDKLDPSDEMS 3681

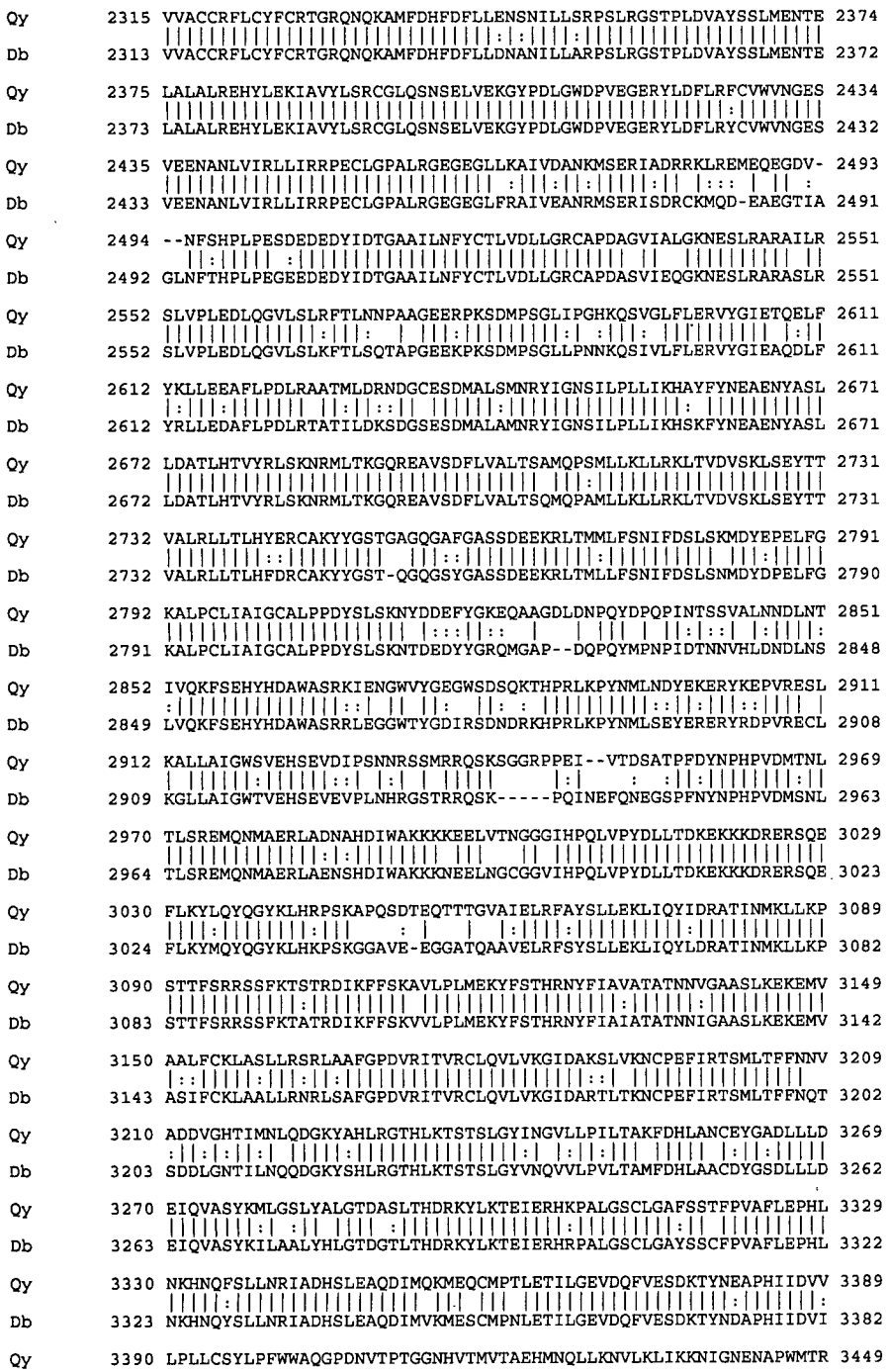




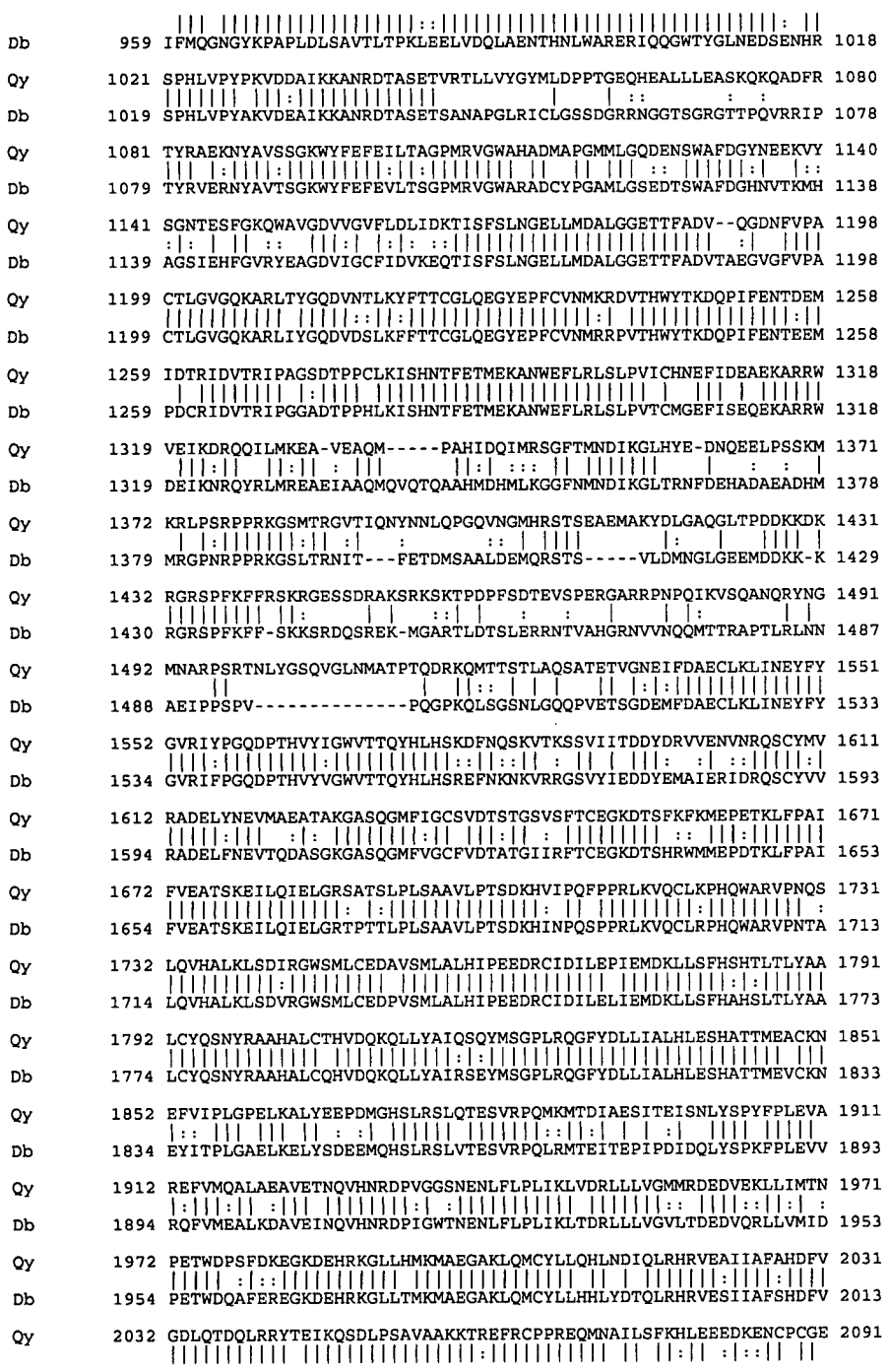
RESULT 14
US-10-668-767-124
; Sequence 124, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 5126
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: gi 2160476
US-10-668-767-124

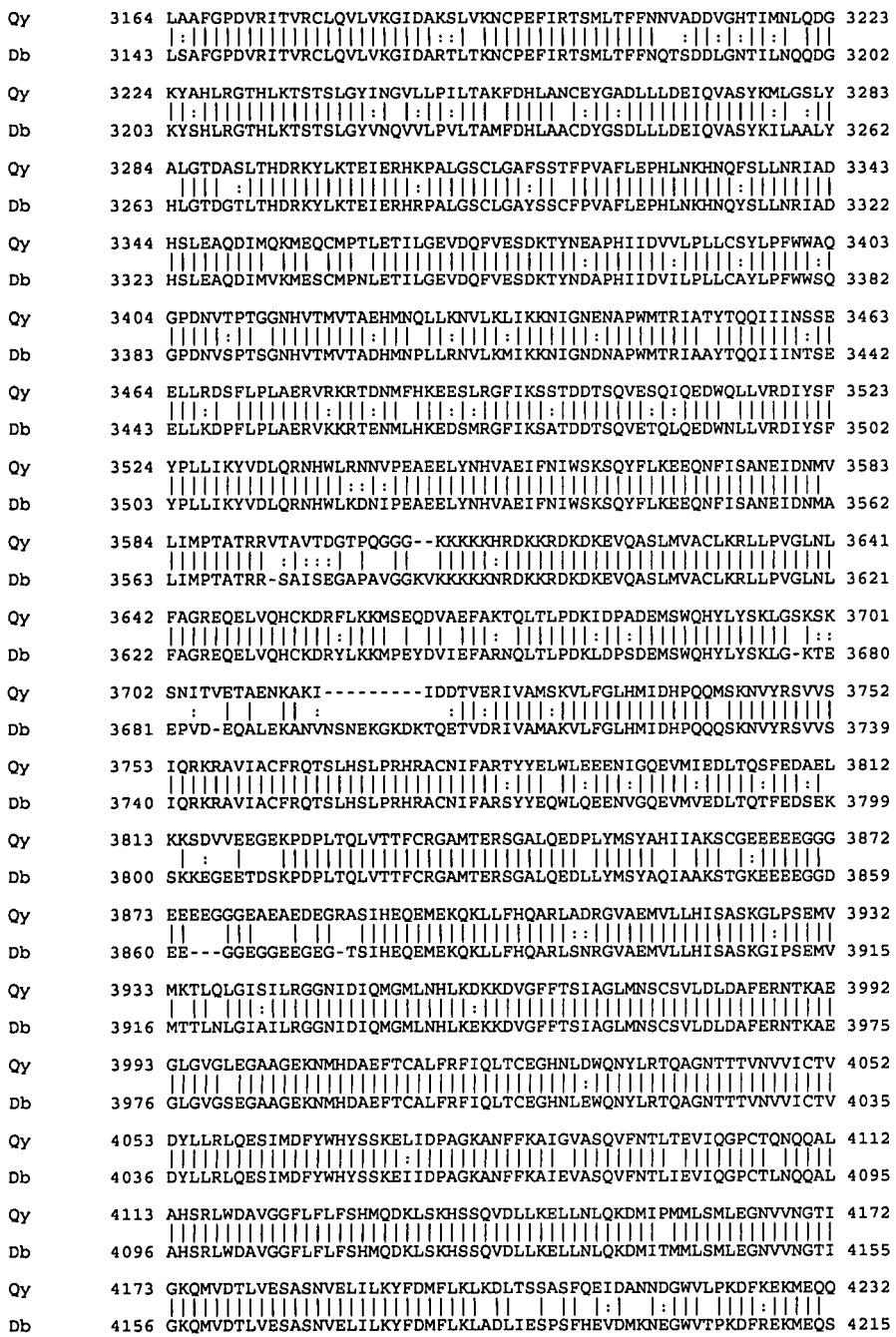
Query Match 79.2%; Score 21218.5; DB 4; Length 5126;
Best Local Similarity 78.6%; Pred. No. 0;
Matches 4072; Conservative 442; Mismatches 545; Indels 123; Gaps 42;

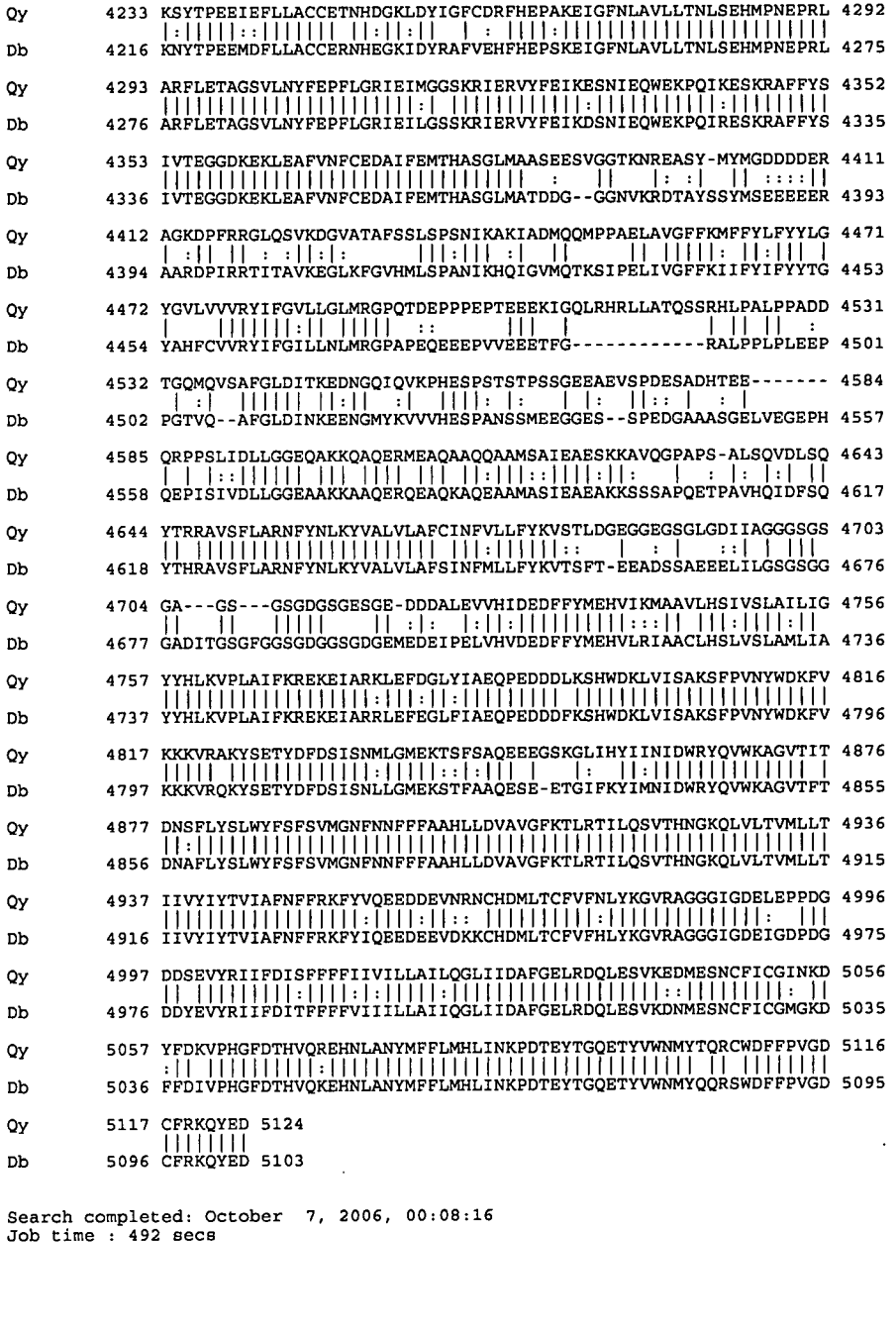



Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2313 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2372
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2433 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2491
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2492 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLR 2551
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2552 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2611
Qy 2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db 2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671
Qy 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731
Qy 2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db 2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
Db 2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848
Qy 2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db 2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908
Qy 2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
Db 2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963
Qy 2970 TLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQE 3029
Db 2964 TLSREMQNMAERLAENSHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQE 3023
Qy 3030 FLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKP 3089
Db 3024 FLKYMQYQGYKLHKPSKGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKP 3082
Qy 3090 STTFSRRSSFKTSTRDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMV 3149
Db 3083 STTFSRRSSFKTATRDIKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMV 3142
Qy 3150 AALFCKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNV 3209
Db 3143 ASIFCKLAALLRNRLSAFGPDVRITVRCLQVLVKGIDARTLTKNCPEFIRTSMLTFFNQT 3202
Qy 3210 ADDVGHTIMNLQDGKYAHLRGTHLKTSTSLGYINGVLLPILTAKFDHLANCEYGADLLLD 3269
Db 3203 SDDLGNTILNQQDGKYSHLRGTHLKTSTSLGYVNQVVLPVLTAMFDHLAACDYGSDLLLD 3262
Qy 3270 EIQVASYKMLGSLYALGTDASLTHDRKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHL 3329
Db 3263 EIQVASYKILAALYHLGTDGTLTHDRKYLKTEIERHRPALGSCLGAYSSCFPVAFLEPHL 3322
Qy 3330 NKHNQFSLLNRIADHSLEAQDIMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVV 3389
Db 3323 NKHNQYSLLNRIADHSLEAQDIMVKMESCMPNLETILGEVDQFVESDKTYNDAPHIIDVI 3382
Qy 3390 LPLLCSYLPFWWAQGPDNVTPTGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTR 3449
Db 3383 LPLLCAYLPFWWSQGPDNVSPTSGNHVTMVTADHMNPLLRNVLKMIKKNIGNDNAPWMTR 3442
Qy 3450 IATYTQQIIINSSEELLRDSFLPLAERVRKRTDNMFHKEESLRGFIKSSTDDTSQVESQI 3509
Db 3443 IAAYTQQIIINTSEELLKDPFLPLAERVKKRTENMLHKEDSMRGFIKSATDDTSQVETQL 3502
Qy 3510 QEDWQLLVRDIYSFYPLLIKYVDLQRNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKE 3569
Db 3503 QEDWNLLVRDIYSFYPLLIKYVDLQRNHWLKDNIPEAEELYNHVAEIFNIWSKSQYFLKE 3562
Qy 3570 EQNFISANEIDNMVLIMPTATRRVTAVTDGTPQGGG--KKKKKHRDKKRDKDKEVQASLM 3627
Db 3563 EQNFISANEIDNMALIMPTATRR-SAISEGAPAVGGKVKKKKKNRDKKRDKDKEVQASLM 3621
Qy 3628 VACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMS 3687
Db 3622 VACLKRLLPVGLNLFAGREQELVQHCKDRYLKKMPEYDVIEFARNQLTLPDKLDPSDEMS 3681
Qy 3688 WQHYLYSKLGSKSKSNITVETAENKAKI---------IDDTVERIVAMSKVLFGLHMIDH 3738
Db 3682 WQHYLYSKLG-KTEEPVD-EQALEKANVNSNEKGKDKTQETVDRIVAMAKVLFGLHMIDH 3739
Qy 3739 PQQMSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEV 3798
Db 3740 PQQQSKNVYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARSYYEQWLQEENVGQEV 3799
Qy 3799 MIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHI 3858
Db 3800 MVEDLTQTFEDSEKSKKEGEETDSKPDPLTQLVTTFCRGAMTERSGALQEDLLYMSYAQI 3859
Qy 3859 IAKSCGEEEEEGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVL 3918
Db 3860 AAKSTGKEEEEGGDEE---GGEGGEEGEG-TSIHEQEMEKQKLLFHQARLSNRGVAEMVL 3915
Qy 3919 LHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNSCS 3978
Db 3916 LHISASKGIPSEMVMTTLNLGIAILRGGNIDIQMGMLNHLKEKKDVGFFTSIAGLMNSCS 3975
Qy 3979 VLDLDAFERNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQ 4038
Db 3976 VLDLDAFERNTKAEGLGVGSEGAAGEKNMHDAEFTCALFRFIQLTCEGHNLEWQNYLRTQ 4035
Qy 4039 AGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNTLT 4098
Db 4036 AGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKEIIDPAGKANFFKAIEVASQVFNTLI 4095
Qy 4099 EVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPM 4158
Db 4096 EVIQGPCTLNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITM 4155
Qy 4159 MLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDG 4218
Db 4156 MLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLADLIESPSFHEVDMKNEG 4215
Qy 4219 WVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPAKEIGFNLAVL 4278
Db 4216 WVTPKDFREKMEQSKNYTPEEMDFLLACCERNHEGKIDYRAFVEHFHEPSKEIGFNLAVL 4275
Qy 4279 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWE 4338
Db 4276 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEILGSSKRIERVYFEIKDSNIEQWE 4335
Qy 4339 KPQIKESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNRE 4398
Db 4336 KPQIRESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRD 4393
Qy 4399 ASY-MYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAV 4457
Db 4394 TAYSSYMSEEEEERAARDPIRRTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIV 4453
Qy 4458 GFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLAT 4517

```
Db       4454 GFFKIIFYIFYYTGYAHFCVVRYIFGILLNLMRGPAPEQEEEPVVEEETFG--------- 4504

Qy       4518 QSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDE 4577

Db       4505 ---RALPPLPLEEPPGTVQ--AFGLDINKEENGMYKVVVHESPANSSMEEGGES--SPED 4557

Qy       4578 SADHTEE-------QRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQG 4630

Db       4558 GAAASGELVEGEPHQEPISIVDLLGGEAAKKAAQERQEAQKAQEAAMASIEAEAKKSSSA 4617

Qy       4631 PAPS-ALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEG 4689

Db       4618 PQETPAVHQIDFSQYTHRAVSFLARNFYNLKYVALVLAFSINFMLLFYKVTSFT-EEADS 4676

Qy       4690 SGLGDIIAGGGSGSGA---GS---GSGDGSGESGE-DDDALEVVHIDEDFFYMEHVIKMA 4742

Db       4677 SAEEELILGSGSGGGADITGSGFGGSGDGGSGDGEMEDEIPELVHVDEDFFYMEHVLRIA 4736

Qy       4743 AVLHSIVSLAILIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKLVI 4802

Db       4737 ACLHSLVSLAMLIAYYHLKVPLAIFKREKEIARRLEFEGLFIAEQPEDDDFKSHWDKLVI 4796

Qy       4803 SAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINI 4862

Db       4797 SAKSFPVNYWDKFVKKKVRQKYSETYDFDSISNLLGMEKSTFAAQESE-ETGIFKYIMNI 4855

Qy       4863 DWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVT 4922

Db       4856 DWRYQVWKAGVTFTDNAFLYSLWYFSFSVMGNFNNFFFAAHLLDVAVGFKTLRTILQSVT 4915

Qy       4923 HNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYVQEEDDEVNRNCHDMLTCFVFNLYKGVR 4982

Db       4916 HNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYIQEEDEEVDKKCHDMLTCFVFHLYKGVR 4975

Qy       4983 AGGGIGDELEPPDGDDSEVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVKE 5042

Db       4976 AGGGIGDEIGDPDGDDYEVYRIIFDITFFFFVIIILLAIIQGLIIDAFGELRDQLESVKD 5035

Qy       5043 DMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVWN 5102

Db       5036 NMESNCFICGMGKDFFDIVPHGFDTHVQKEHNLANYMFFLMHLINKPDTEYTGQETYVWN 5095

Qy       5103 MYTQRCWDFFPVGDCFRKQYED 5124

Db       5096 MYQQRSWDFFPVGDCFRKQYED 5117


RESULT 15
US-10-668-767-126
; Sequence 126, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
;   LENGTH: 5112
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: gi 2160478
US-10-668-767-126

  Query Match            79.1%;  Score 21191.5;  DB 4;  Length 5112;
  Best Local Similarity  78.6%;  Pred. No. 0;
  Matches 4061;  Conservative  450;  Mismatches  548;  Indels  109;  Gaps   41;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Db        659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780

Db        719 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Db        779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Db        839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Db        899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
```


Db 959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1019 SPHLVPYAKVDEAIKKANRDTASETSANAPGLRICLGSSDGRRNGGTSGRGTTPQVRRIP 1078
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1138
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1139 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1258
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1488 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1714 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1773
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1774 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1833
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1893
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1894 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1953
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1954 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFV 2013
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2014 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2073
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
Db 2074 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2133
Qy 2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db 2134 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2193
Qy 2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db 2194 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2253
Qy 2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db 2254 RVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2312
Qy 2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db 2313 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2372
Qy 2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db 2373 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIR 2432
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db 2433 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2491
Qy 2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db 2492 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLRSLVPLEDLQGVLSL 2551
Qy 2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db 2552 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2611
Qy 2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
Db 2612 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2671
Qy 2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db 2672 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2731
Qy 2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db 2732 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2790
Qy 2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db 2791 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2848
Qy 2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db 2849 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2908
Qy 2926 VDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLA 2983
Db 2909 VEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLA 2963
Qy 2984 DNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHR 3043
Db 2964 ENSHDIWAKKKNEELNGCGGVIHPQLVPYDLLTDKEKKKDRERSQEFLKYMQYQGYKLHK 3023
Qy 3044 PSKAPQSDTEQTTTGVAIELRFAYSLLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTST 3103
Db 3024 PSKGGAVE-EGGATQAAVELRFSYSLLEKLIQYLDRATINMKLLKPSTTFSRRSSFKTAT 3082
Qy 3104 RDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSR 3163
Db 3083 RDIKFFSKVVLPLMEKYFSTHRNYFIAIATATNNIGAASLKEKEMVASIFCKLAALLRNR 3142





Search completed: October 7, 2006, 00:08:16
Job time : 492 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 7, 2006, 00:02:14 ; Search time 92 Seconds
(without alignments)
4399.726 Million cell updates/sec

Title: US-10-668-767-128
Perfect score: 26800
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....WDFFPVGDCFRKQYEDLMGE 5128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 291792 seqs, 78934247 residues

Total number of hits satisfying chosen parameters: 291792

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	662.5	2.5	2764	6	US-10-570-909-16	Sequence 16, Appl
2	601.5	2.2	2671	6	US-10-505-928-784	Sequence 784, App
3	591.5	2.2	2639	7	US-11-343-271-31	Sequence 31, Appl
4	304.5	1.1	3913	7	US-11-090-997-870	Sequence 870, App
5	301.5	1.1	3842	7	US-11-090-997-876	Sequence 876, App
6	301.5	1.1	3896	7	US-11-090-997-872	Sequence 872, App
7	301.5	1.1	3907	7	US-11-090-997-868	Sequence 868, App
8	283	1.1	3113	6	US-10-505-928-325	Sequence 325, App
9	253.5	0.9	3811	7	US-11-090-997-10	Sequence 10, Appl
10	224.5	0.8	5001	7	US-11-070-573-68	Sequence 68, Appl
11	219	0.8	1703	7	US-11-056-355B-86482	Sequence 86482, A
12	219	0.8	1710	7	US-11-056-355B-86481	Sequence 86481, A
13	219	0.8	1744	7	US-11-056-355B-86480	Sequence 86480, A
14	208.5	0.8	3429	6	US-10-953-349-9275	Sequence 9275, Ap
15	208.5	0.8	3438	6	US-10-953-349-9274	Sequence 9274, Ap
16	208.5	0.8	3478	6	US-10-953-349-9273	Sequence 9273, Ap
17	208	0.8	1828	7	US-11-056-355B-91730	Sequence 91730, A
18	208	0.8	1828	7	US-11-056-355B-95486	Sequence 95486, A
19	208	0.8	1999	7	US-11-056-355B-91729	Sequence 91729, A
20	208	0.8	1999	7	US-11-056-355B-95485	Sequence 95485, A
21	208	0.8	2008	7	US-11-056-355B-91728	Sequence 91728, A
22	208	0.8	2008	7	US-11-056-355B-95484	Sequence 95484, A
23	197.5	0.7	9535	6	US-10-471-571A-4496	Sequence 4496, Ap
24	193.5	0.7	2304	6	US-10-540-898-310	Sequence 310, App
25	189.5	0.7	1626	7	US-11-090-997-874	Sequence 874, App
26	184	0.7	1314	7	US-11-293-697-3679	Sequence 3679, Ap
27	183	0.7	2649	7	US-11-188-417A-25	Sequence 25, Appl
28	179	0.7	2890	6	US-10-553-928-279	Sequence 279, App
29	174.5	0.7	1575	6	US-10-505-928-257	Sequence 257, App
30	174.5	0.7	2364	7	US-11-289-102-242	Sequence 242, App
31	171.5	0.6	1328	6	US-10-504-973-32	Sequence 32, Appl
32	171	0.6	1416	7	US-11-090-997-1692	Sequence 1692, Ap
33	171	0.6	1663	6	US-10-505-928-227	Sequence 227, App
34	169.5	0.6	5183	7	US-11-090-997-1562	Sequence 1562, Ap
35	169	0.6	2274	7	US-11-434-137-9930	Sequence 9930, Ap
36	169	0.6	2274	7	US-11-434-184-9930	Sequence 9930, Ap
37	169	0.6	2274	7	US-11-434-199-9930	Sequence 9930, Ap
38	169	0.6	2274	7	US-11-434-203-9930	Sequence 9930, Ap
39	169	0.6	2278	7	US-11-434-137-5856	Sequence 5856, Ap
40	169	0.6	2278	7	US-11-434-184-5856	Sequence 5856, Ap
41	169	0.6	2278	7	US-11-434-199-5856	Sequence 5856, Ap
42	169	0.6	2278	7	US-11-434-203-5856	Sequence 5856, Ap
43	168	0.6	824	7	US-11-090-997-1030	Sequence 1030, Ap
44	168	0.6	855	7	US-11-090-997-1028	Sequence 1028, Ap
45	166.5	0.6	2871	6	US-10-505-928-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-10-570-909-16
; Sequence 16, Application US/10570909
; Publication No. US20060216292A1
; GENERAL INFORMATION:
; APPLICANT: Hopf, Carsten
; TITLE OF INVENTION: Treatment of Neurodegenerative Diseases
; FILE REFERENCE: 14129-00001-US
; CURRENT APPLICATION NUMBER: US/10/570,909
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: PCT/EP2004/009771
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: EP 03019642.2
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/EP2003/013980
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: EP 04001895.4
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: EP 04001894.7
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: EP 04007447.8
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/EP2004/004891
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: PCT/EP2004/004889
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: EP 04018874.0
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 2764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-570-909-16

Query Match 2.5%; Score 662.5; DB 6; Length 2764;
Best Local Similarity 17.7%; Pred. No. 1.5e-31;
Matches 673; Conservative 490; Mismatches 1070; Indels 1559; Gaps 162;

```
Qy       1753 VSMLALHIPEEDRCI------DILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCT 1806
                :| | |    :|||:      |: | :  :  |              || : | |
Db         27 ISTLGL---VDDRCVVQPETGDLNNPPKKFRDCLF---------KLCPMNRYSA------ 68

Qy       1807 HVDQKQLLYAIQSQYMSGPLRQGFYD--LLIALHLESHATTMEACKNE--------FVIP 1856
                |||   | :      |       |  ||  ||   ||  :|  :||          ||
Db         69 ---QKQFWKAAK------PGANSTTDAVLLNKLH---HAADLEKKQNETENRKLLGTVIQ 116
```

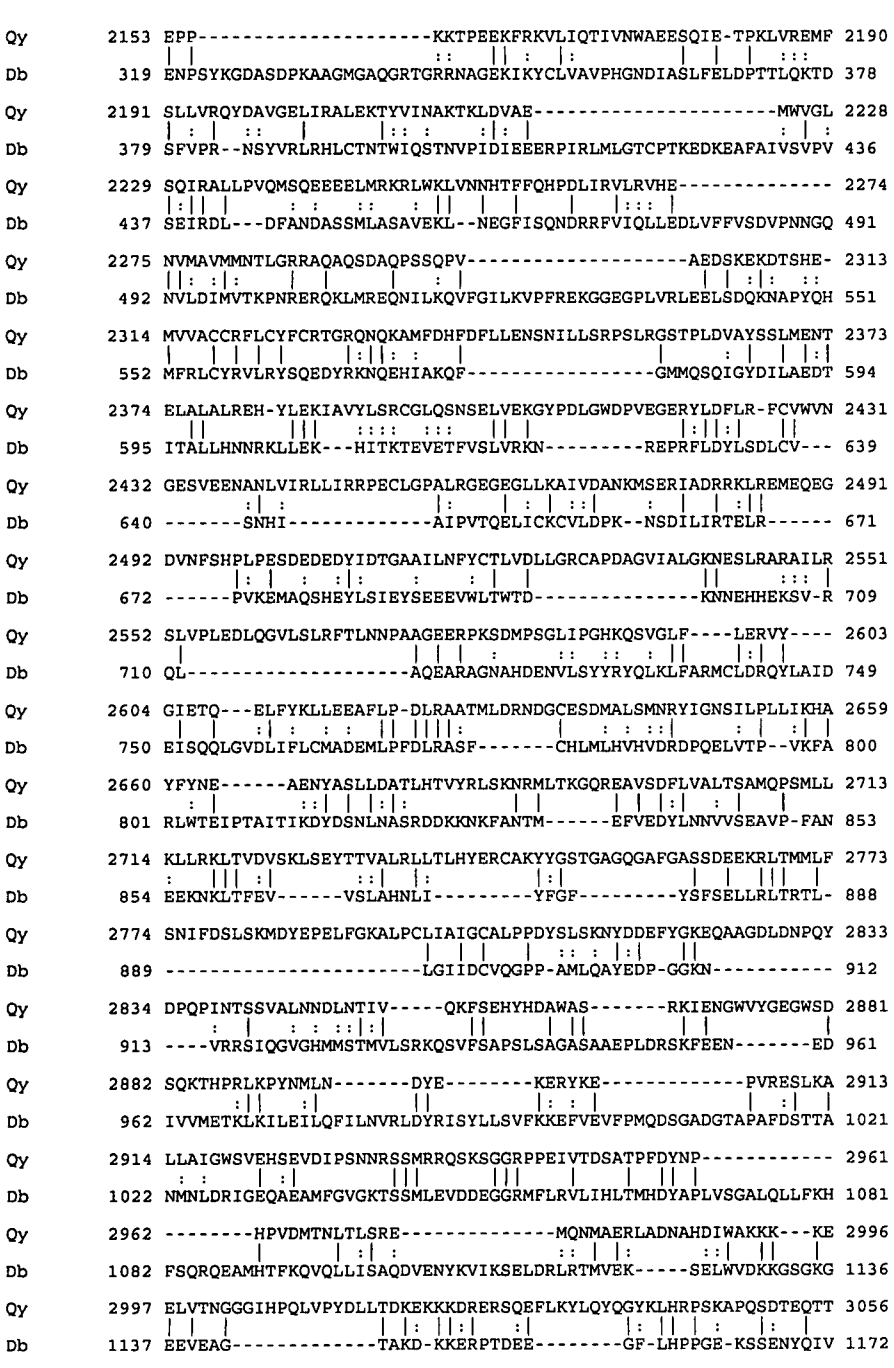
```
Db       1664 GGFICKLIKHTKQLLEENEEKLCIKVLQTLREMMTKDRGYGEKLISID---ELDNAELPP 1720

Qy       3813 --KKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEE-- 3868

Db       1721 APDSENATEELEPSPPLRQLED-------HKRGEALRQVLVNRYYGNV--RPSGRRESLT 1771

Qy       3869 -------EGGGEEEEGGGEAEAEDEGRASIHEQEMEKQKLLFHQARLADRGVAEMVL-LH 3920

Db       1772 SFGNGPLSAGGPGKPGGG---GGGSGSSSMSRGEMSLAEV---QCHLDKEGASNLVIDLI 1825

Qy       3921 ISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHL-KDKKDVGFF------------ 3967

Db       1826 MNASS---DRVFHESILLAIALLEGGNTTIQHSFFCRLTEDKKSEKFFKVFYDRMKVAQQ 1882

Qy       3968 ---------TSIAGLMNSCSVLDLDAFERNTKAEGL------------------------ 3994

Db       1883 EIKATVTVNTSDLGNKKKDDEVDRDAPSRKKAKEPTTQITEEVRDQLLEASAATRKAFTT 1942

Qy       3995 ------------GVGLEGAAGEKNMHDAEFTCA------LFRFIQLTCEGHNLDWQNYL 4035

Db       1943 FRREADPDDHYQPGEGTQ-ATADKAKDDLEMSAVITIMQPILRFLQLLCENHNRDLQNFL 2001

Qy       4036 RTQAGNTTTVNVVICTVDYLLRLQES------IMDFYWHYSSKELIDPAGKANFFKAIGV 4089

Db       2002 RCQ-NNKTNYNLVCETLQFLDCICGSTTGGLGLLGLYINE--------------KNVAL 2045

Qy       4090 ASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELL 4149

Db       2046 INQTLESLTEYCQGPCHENQNCIA----------------------THESNGIDIITAL- 2082

Qy       4150 NLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVE-SASNVELILKYFDMFLKLKDLTSSAS 4208

Db       2083 -ILNDINP-------------LGKKRMDLVLELKAKNASKLL-----LAIMESRHDSEN 2122

Qy       4209 FQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPA 4268

Db       2123 AERILYN----MRPKELVEVI--KKAYMQGEVEF-----EDGENGE-------DGAASP- 2163

Qy       4269 KEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSV-----LNYFEPFLGRIEIMGGSKRIE 4323

Db       2164 RNVGHNIYILAHQLARH---NKELQSMLKPGGQVDGDEALEFYAKHTAQIEIVRLDRTME 2220

Qy       4324 RVYFEIKESNIEQWEKPQI-----KESKRAFFYSIVTEGGDK-EKLEAFVNFCEDAIFEM 4377

Db       2221 QIVFPV----------PSICEFLTKESKLRIYYT--TERDEQGSKINDFFLRSEDLFNEM 2268

Qy       4378 THASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSP 4437

Db       2269 NWQKKLRA----------------------------------QPVLYWCARNMSFW-- 2290

Qy       4438 SNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEP 4497

Db       2291 SSISFNLAVLMNLLVA---------FFYPFKGVRGGTL---------------------- 2319

Qy       4498 PPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQVSAFGLDITKEDNGQIQVKPH 4557

Db       2320 ------------------------------------------------------------EPH 2322

Qy       4558 ESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAM 4617

Db       2323 WS---------------------------------------------------------- 2324

Qy       4618 SAIEAESKKAVQGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLLFY 4677

Db       2325 ------------------------------------GLLWTAMLISLAIVIAL--- 2341

Qy       4678 KVSTLDGEGGEGSGLGDIIAGGGSGSGAGSGSGDGSGESGEDDDALEVVHIDEDFFYMEH 4737

Db       2342 ---------PKPHGIRALIA---------------------------------------- 2352

Qy       4738 VIKMAAVLHSIVSLAI-----LIGYYHLKVPLAIFKREKEIARKLEFDGLYIAEQPEDDD 4792

Db       2353 ----STILRLIFSVGLQPTLFLLGAFN-------------VCNKIIF------------- 2382
```

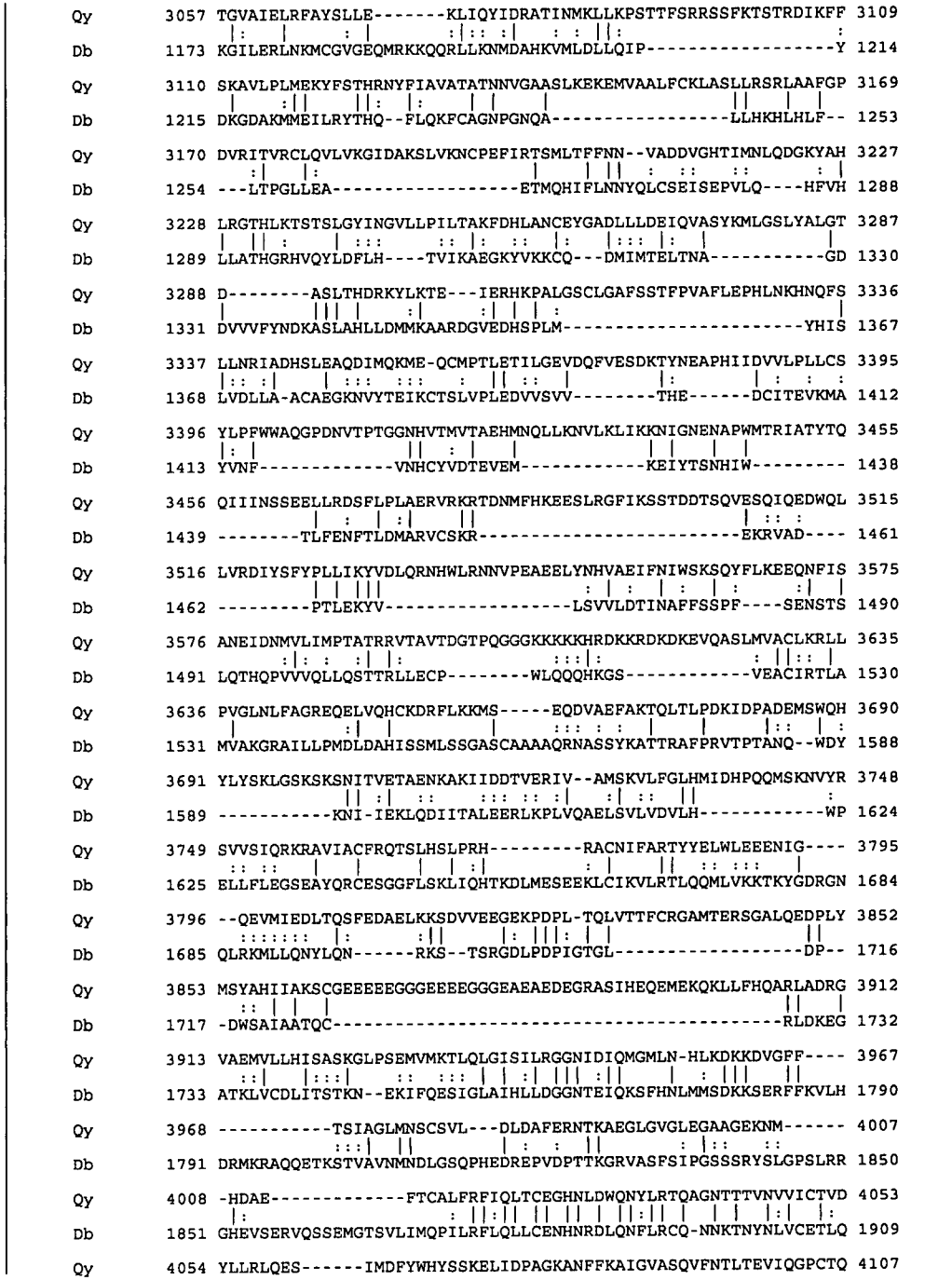
```
Qy       4793 LKSHWDKLVISAKSFPVNYWDKFVKKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGS 4852

Db       2383 ------------------------------------------------------------ 2382

Qy       4853 KGLIHYIINIDWRYQVWKAGVTITDNSFLYSLWYFSFSVMGNF-NNFFFAAHLLDVAVGF 4911

Db       2383 --LMSFVGNCGTFTRGYRA--MVLDVEFLYHLLYLVICAMGLFVHEFFYSLLLFDLVYRE 2438

Qy       4912 KTLRTILQSVTHNGKQLVLTVMLLTIIVYIYTVIAFNFFRKFYV---------------- 4955

Db       2439 ETLLNVIKSVTRNGRSIILTAVLALILVYLFSIVGYLFFKDDFILEVDRLPNETAVPETG 2498

Qy       4956 --------------------------------QEEDDEVNRNCHDMLTCFVFNLYKGVR 4982

Db       2499 ESLASEFLFSDVCRVESGENCSSPAPREELVPAEETEQDKEHTCETLLMCIVTVLSHGLR 2558

Qy       4983 AGGGIGDELEPPDGDDS-EVYRIIFDISFFFFIIVILLAILQGLIIDAFGELRDQLESVK 5041

Db       2559 SGGGVGDVLRKPSKEEPLFAARVIYDLLFFFMVIIIVLNLIFGVIIDTFADLRSEKQKKE 2618

Qy       5042 EDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTEYTGQETYVW 5101

Db       2619 EILKTTCFICGLERDKFDNKTVTFEEHIKEEHNMWHYLCFIVLVKVKDSTEYTGPESYVA 2678

Qy       5102 NMYTQRCWDFFP 5113

Db       2679 EMIKERNLDWFP 2690
```

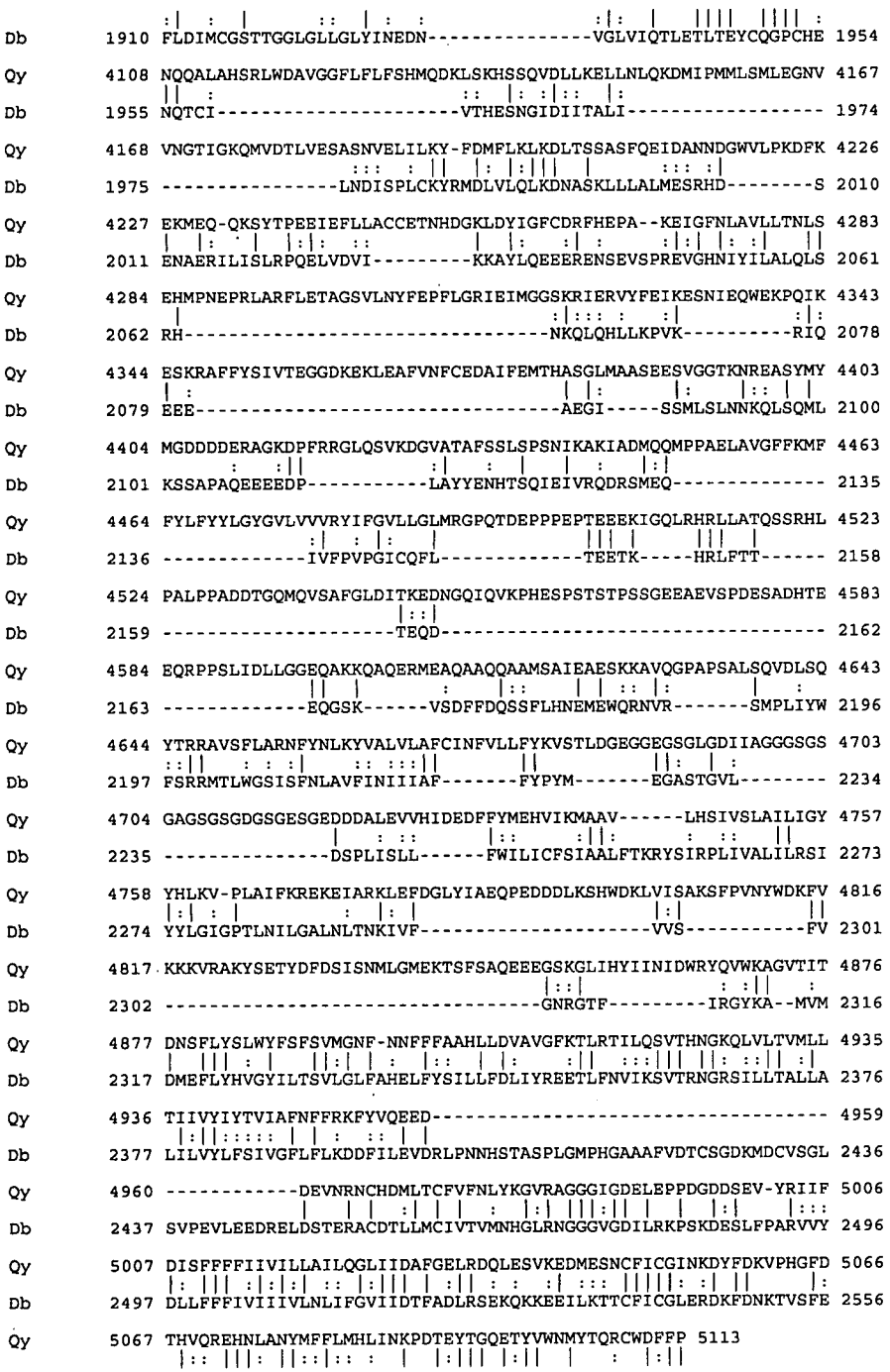
RESULT 2
US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 784
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-784

Query Match 2.2%; Score 601.5; DB 6; Length 2671;
Best Local Similarity 17.4%; Pred. No. 9.2e-28;
Matches 625; Conservative 475; Mismatches 1060; Indels 1427; Gaps 149;

```
Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGL 1991

Db         39 EPAAGDLDN---PPKKFRDCLFKVCPMNRYSAQK-------QYWKAKQTKQDKEKIADVV 88

Qy       1992 LHMKMAEGAKLQMCYLLQHLND----------------IQLRH-----------RVEAII 2024

Db         89 LLQKLQHAAQME-----QKQNDTENKKVHGDVVKYGSVIQLLHMKSNKYLTVNKRLPALL 143

Qy       2025 ------------------AFAHDF-----------VGD---LQTDQLRRYTEIKQSDLPS 2052

Db        144 EKNAMRVTLDATGNEGSWLFIQPFWKLRSNGDNVVVGDKVILNPVNAGQPLHASNYELSD 203

Qy       2053 AVAAKKTREFRCPPREQMNAILSFK-HLEE------------EDKENCPCGEELIARMN 2098

Db        204 NAGCKEVNSVNCNTSWKINLFMQFRDHLEEVLKGGDVVRLFHAEQEKFLTC-DEYKGKLQ 262

Qy       2099 EFHDTLM-----AHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEE-EAKAIE 2152

Db        263 VFLRTTLRQSATSATSSNALWEVEVVHHDPCRGGAGHWNGLYRF----KHLATGNYLAAE 318
```







Db 1910 FLDIMCGSTTGGLGLLGLYINEDN----------VGLVIQTLETLTEYCQGPCHE 1954

Qy 4108 NQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMIPMMLSMLEGNV 4167

Db 1955 NQTCI----------VTHESNGIDIITALI---------- 1974

Qy 4168 VNGTIGKQMVDTLVESASNVELILKY-FDMFLKLKDLTSSASFQEIDANNDGWVLPKDFK 4226

Db 1975 ----------LNDISPLCKYRMDLVLQLKDNASKLLLALMESRHD--------S 2010

Qy 4227 EKMEQ-QKSYTPEEIEFLLACCETNHDGKLDYIGFCDRFHEPA--KEIGFNLAVLLTNLS 4283

Db 2011 ENAERILISLRPQELVDVI---------KKAYLQEEERENSEVSPREVGHNIYILALQLS 2061

Qy 4284 EHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQIK 4343

Db 2062 RH----------NKQLQHLLKPVK----------RIQ 2078

Qy 4344 ESKRAFFYSIVTEGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMY 4403

Db 2079 EEE----------AEGI-----SSMLSLNNKQLSQML 2100

Qy 4404 MGDDDDERAGKDPFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMF 4463

Db 2101 KSSAPAQEEEEDP----------LAYYENHTSQIEIVRQDRSMEQ---------- 2135

Qy 4464 FYLFYYLGYGVLVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHL 4523

Db 2136 ----------IVFPVPGICQFL----------TEETK-----HRLFTT------ 2158

Qy 4524 PALPPADDTGQMQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTE 4583

Db 2159 ----------TEQD---------- 2162

Qy 4584 EQRPPSLIDLLGGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQGPAPSALSQVDLSQ 4643

Db 2163 ----------EQGSK------VSDFFDQSSFLHNEMEWQRNVR-------SMPLIYW 2196

Qy 4644 YTRRAVSFLARNFYNLKYVALVLAFCINFVLLFYKVSTLDGEGGEGSGLGDIIAGGGSGS 4703

Db 2197 FSRRMTLWGSISFNLAVFINIIIAF-------FYPYM-------EGASTGVL-------- 2234

Qy 4704 GAGSGSGDGSGESGEDDDALEVVHIDEDFFYMEHVIKMAAV------LHSIVSLAILIGY 4757

Db 2235 ----------DSPLISLL------FWILICFSIAALFTKRYSIRPLIVALILRSI 2273

Qy 4758 YHLKV-PLAIFKREKEIARKLEFDGLYIAEQPEDDDLKSHWDKLVISAKSFPVNYWDKFV 4816

Db 2274 YYLGIGPTLNILGALNLTNKIVF----------VVS----------FV 2301

Qy 4817 KKKVRAKYSETYDFDSISNMLGMEKTSFSAQEEEGSKGLIHYIINIDWRYQVWKAGVTIT 4876

Db 2302 ----------GNRGTF---------IRGYKA--MVM 2316

Qy 4877 DNSFLYSLWYFSFSVMGNF-NNFFFAAHLLDVAVGFKTLRTILQSVTHNGKQLVLTVMLL 4935

Db 2317 DMEFLYHVGYILTSVLGLFAHELFYSILLFDLIYREETLFNVIKSVTRNGRSILLTALLA 2376

Qy 4936 TIIVYIYTVIAFNFFRKFYVQEED---------- 4959

Db 2377 LILVYLFSIVGFLFLKDDFILEVDRLPNNHSTASPLGMPHGAAAFVDTCSGDKMDCVSGL 2436

Qy 4960 ----------DEVNRNCHDMLTCFVFNLYKGVRAGGGIGDELEPPDGDDSEV-YRIIF 5006

Db 2437 SVPEVLEEDRELDSTERACDTLLMCIVTVMNHGLRNGGGVGDILRKPSKDESLFPARVVY 2496

Qy 5007 DISFFFFIIVILLAILQGLIIDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHGFD 5066

Db 2497 DLLFFFIVIIIVLNLIFGVIIDTFADLRSEKQKKEEILKTTCFICGLERDKFDNKTVSFE 2556

Qy 5067 THVQREHNLANYMFFLMHLINKPDTEYTGQETYVWNMYTQRCWDFFP 5113

Db 2557 EHIKLEHNMWNYLYFIVLVRVKNKTDYTGPESYVAQMIKNKNLDWFP 2603

RESULT 3
US-11-343-271-31
; Sequence 31, Application US/11343271
; Publication No. US20060204503A1
; GENERAL INFORMATION:
; APPLICANT: Fitchett, Jonathon
; APPLICANT: Daniels, Mark
; APPLICANT: LaBarre, Mike
; APPLICANT: McLachlan, Karen
; APPLICANT: Rowe, Tony
; APPLICANT: O'Brien, Nicole
; APPLICANT: Cho, Sam
; APPLICANT: Heller, Melissa
; TITLE OF INVENTION: Treatment of Cancer Using Antibodies to Polypeptides
; TITLE OF INVENTION: Differentially Expressed in Human Lung Tumors
; FILE REFERENCE: 2159.0300001/EKS/J-H
; CURRENT APPLICATION NUMBER: US/11/343,271
; CURRENT FILING DATE: 2006-01-31
; PRIOR APPLICATION NUMBER: 60/648,257
; PRIOR FILING DATE: 2005-01-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 2639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-343-271-31

Query Match 2.2%; Score 591.5; DB 7; Length 2639;
Best Local Similarity 17.4%; Pred. No. 3.8e-27;
Matches 646; Conservative 481; Mismatches 1020; Indels 1567; Gaps 155;

Qy 1815 YAIQSQYMSG-PLRQGFYDLLIALHLESHATTMEACKNEF---------- 1853

Db 4 YSAQKQYWKAKQAKQGNHTEAALLKKLQHAAELEQKQNESENKKLLGEIVKYSNVIQLLH 63

Qy 1854 -----VIPLGPELKALYEEPDMGHSLRSLQTES----VRPQMKMTDIAESITEISNLYSP 1904

Db 64 IKSNKYLTVNKRLPALLEKNAMRVSLDAAGNEGSWFYIHPFWKLRSEGDNI--------- 114

Qy 1905 YFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDR---------- 1951

Db 115 ----------VVGDKVVLMPVNAGQPLHASN-------IELLDNPGCKEVNAVNCNT 154

Qy 1952 -----LLLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCY 2006

Db 155 SWKITLFMKYSSYREDVLK----------GGDVVR--LFH---AEQEKFLTCD 192

Qy 2007 LLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPP 2066

Db 193 EYEKKQHIFLR----------TTLRQS-ATSATSSKALWEIEVVH 226

Qy 2067 RE-------QMNAILSFKHLEEEDKENCPCGEELIARMN-EFHDTLMAHVSLHALQEPDA 2118

Db 227 HDPCRGGAGQWNSLFRFKHL--------ATGNYLAAELNPDYRDAQNEGKNVRDGVPPTS 278

Qy 2119 AENQEPEAKPGAFGKLYNII-----NTVKEL-EEEAKAIEEPPKKTPEEKFRKVLIQTIV 2172

Db 279 KKKRQAGEK-----IMYTLVSVPHGNDIASLFELDATTLQRADCLVPRNSYVRLRHLCTN 333

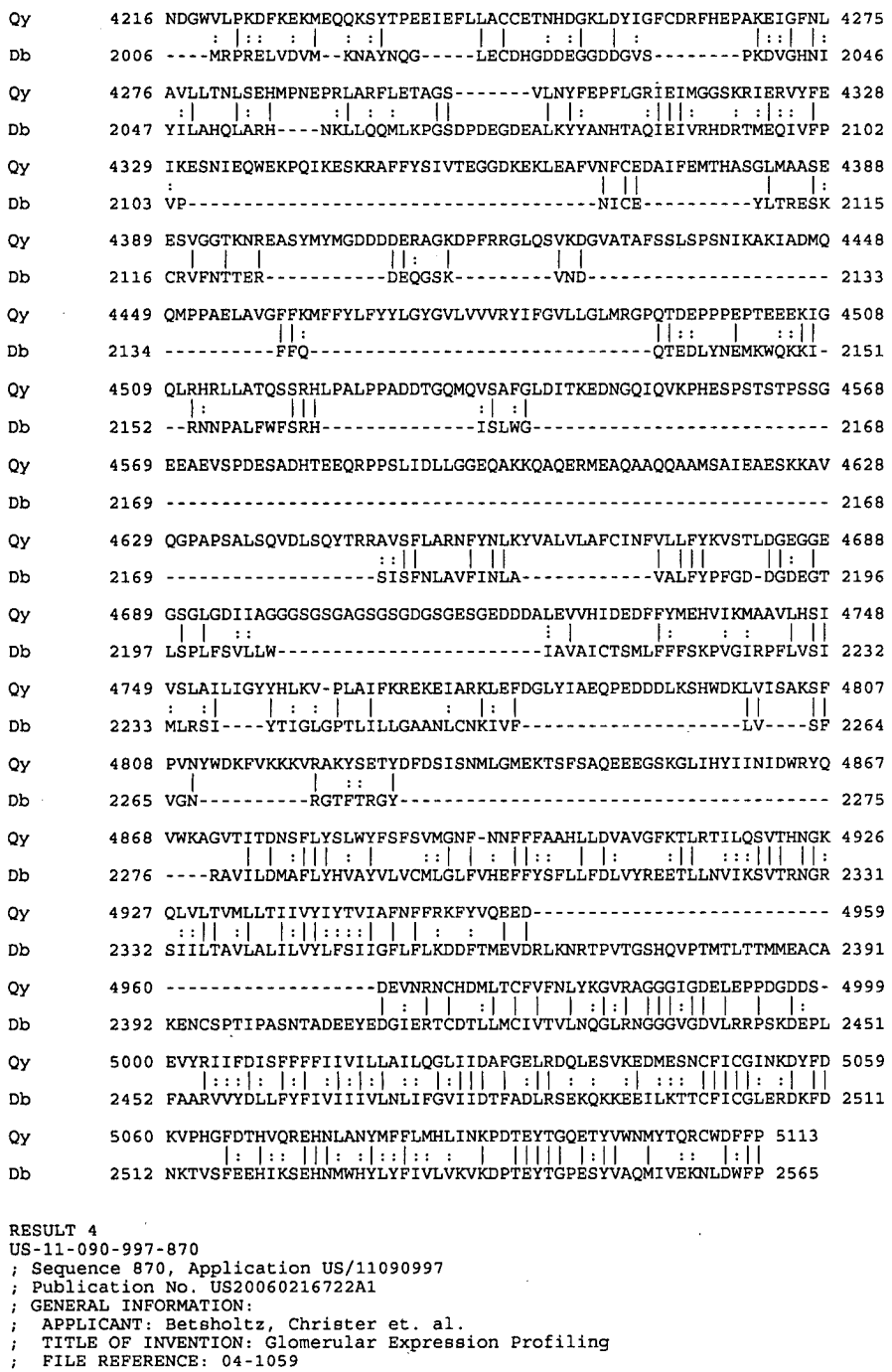
Qy 2173 NWAEESQI------ETPKLV----------REMFSLL------VRQYDAVGELIRAL--- 2207

Db 334 TWVTSTSIPIDTDEERPVMLKIGTCQTKEDKEAFAIVSVPLSEVRDLDFANDANKVLATT 393

Qy 2208 ----------EKTYVINAKTKL------DVAEMWVGLSQIRALLPVQMSQEEEELMRK 2249

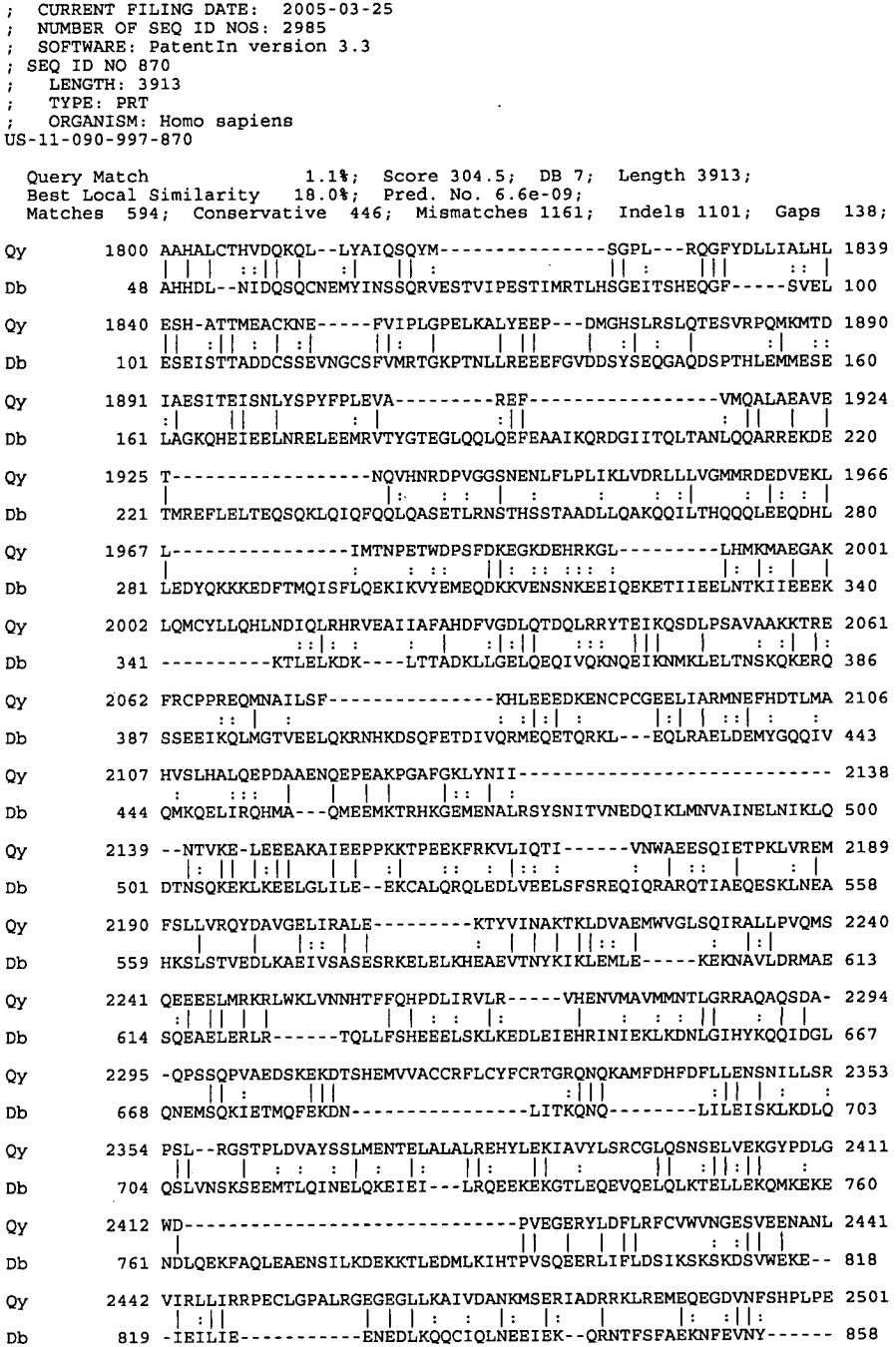
Db 394 VKKLENGTITQNERRFV----TKLLEDLIFFVADVPNNGQEVLDVVITKPNRERQKLMRE 449

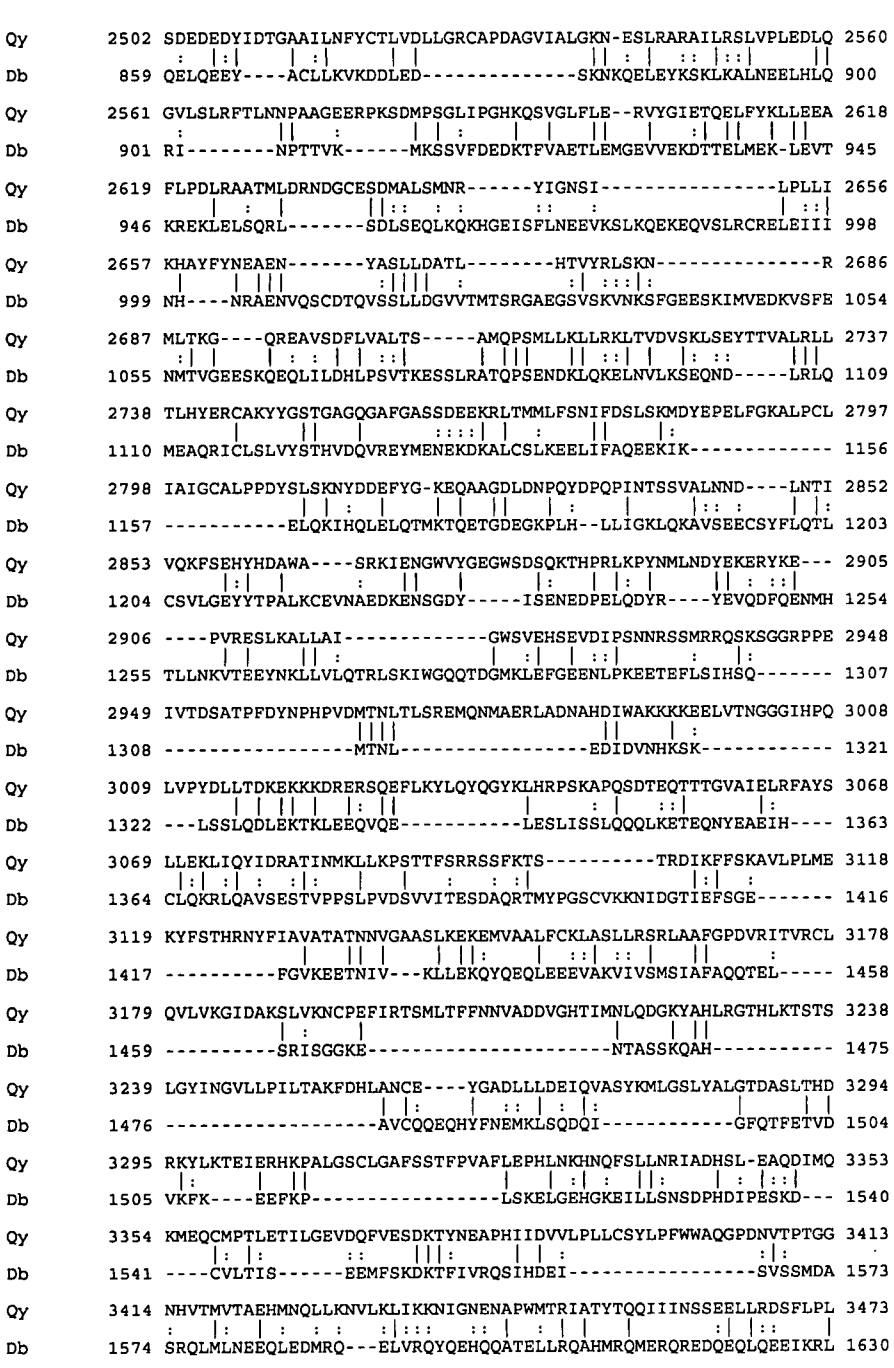
Qy 2250 RLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKD 2309

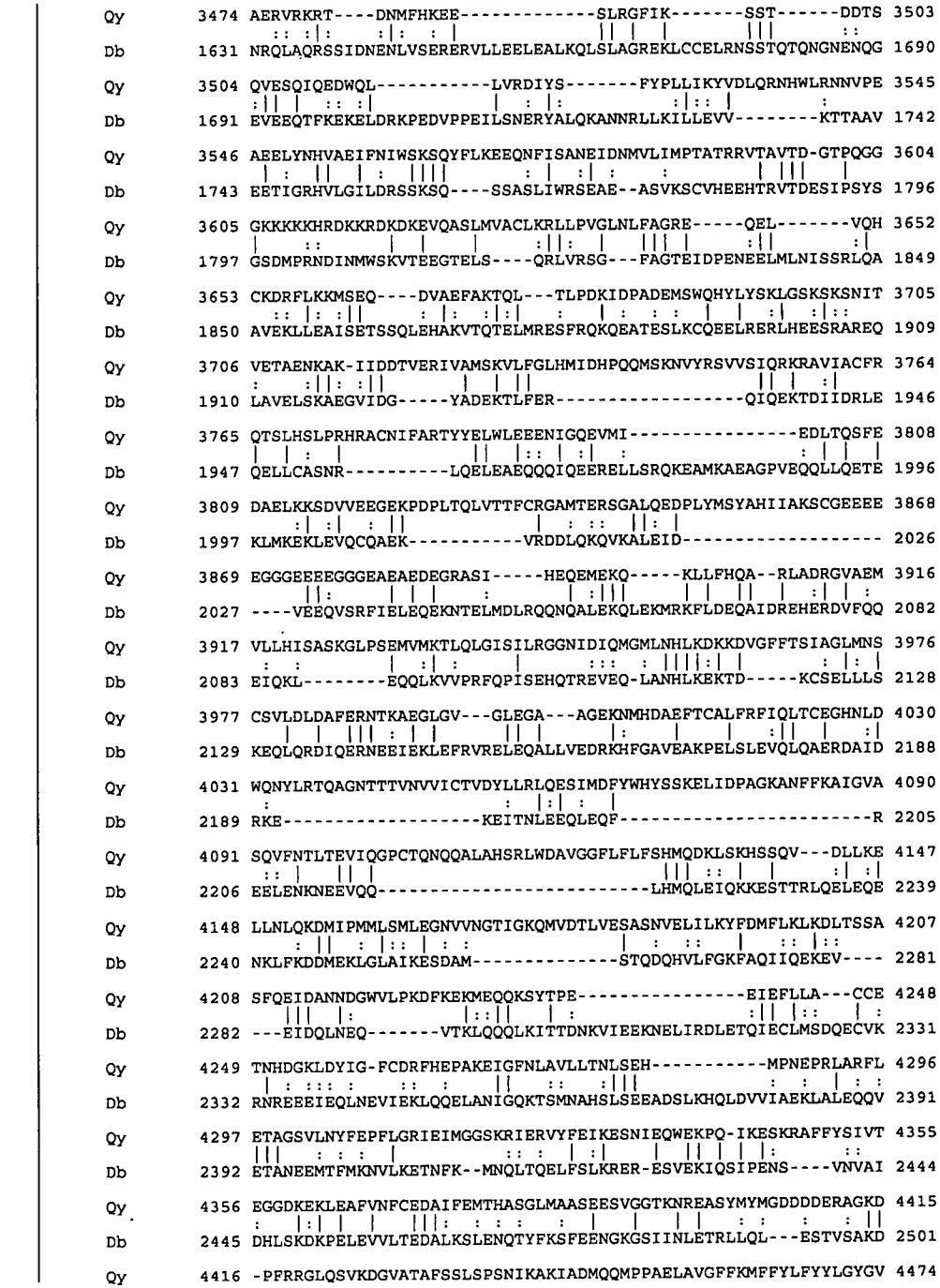


RESULT 4
US-11-090-997-870
; Sequence 870, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 870
; LENGTH: 3913
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-870

Query Match 1.1%; Score 304.5; DB 7; Length 3913;
Best Local Similarity 18.0%; Pred. No. 6.6e-09;
Matches 594; Conservative 446; Mismatches 1161; Indels 1101; Gaps 138;

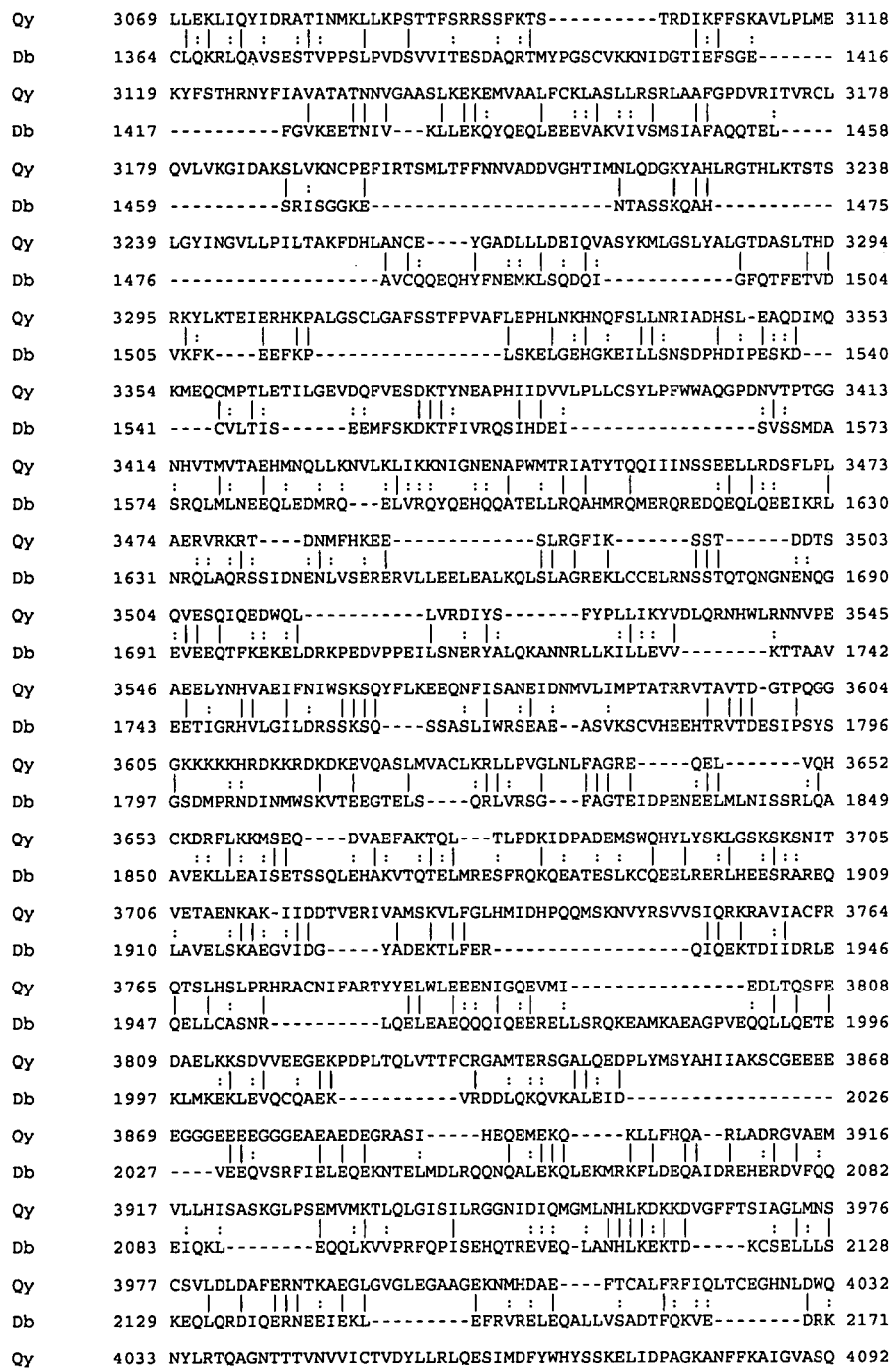


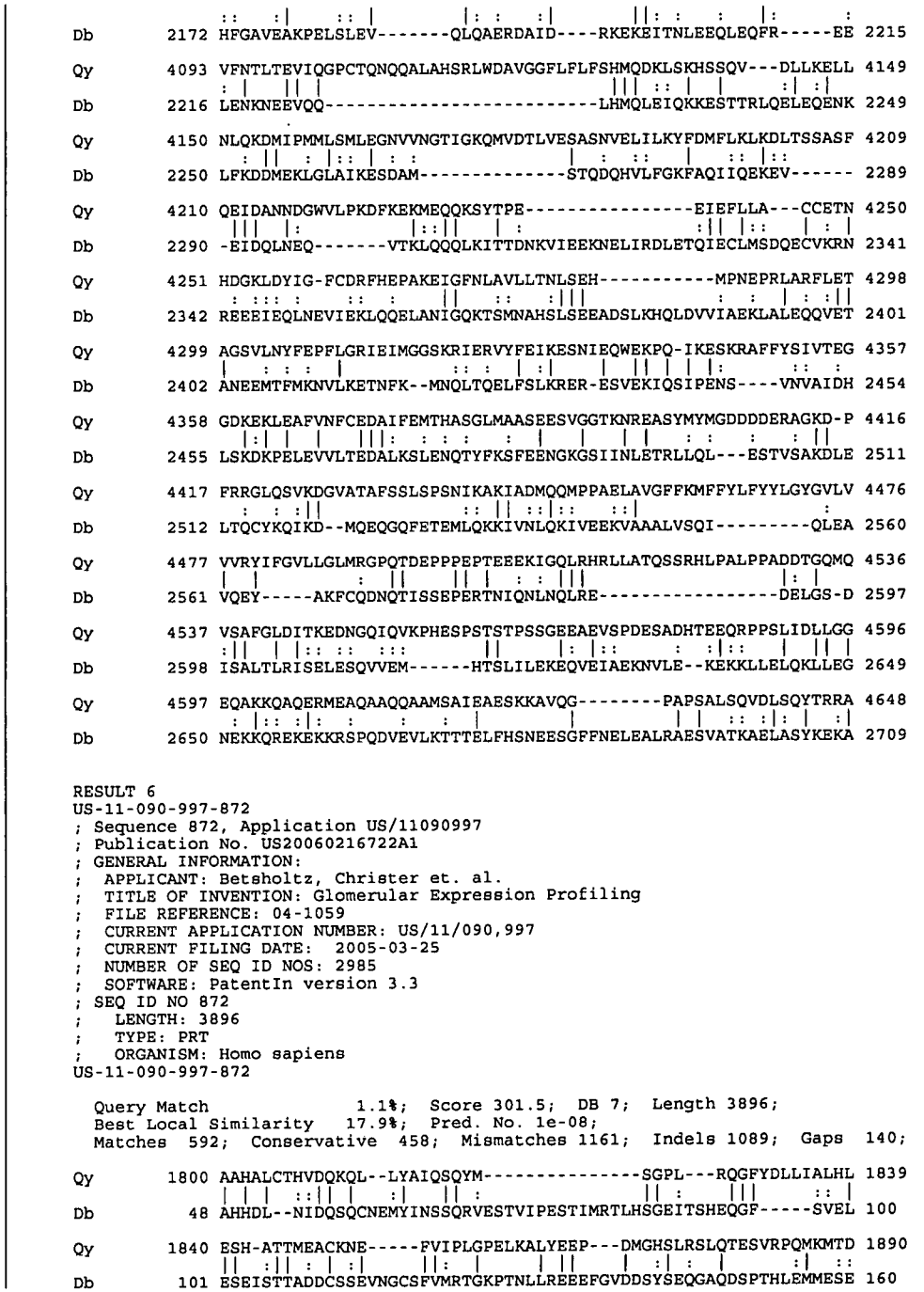

Qy 2502 SDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKN-ESLRARAILRSLVPLEDLQ 2560
Db 859 QELQEEY----ACLLKVKDDLED----------SKNKQELEYKSKLKALNEELHLQ 900
Qy 2561 GVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLE--RVYGIETQELFYKLLEEA 2618
Db 901 RI--------NPTTVK------MKSSVFDEDKTFVAETLEMGEVVEKDTTELMEK-LEVT 945
Qy 2619 FLPDLRAATMLDRNDGCESDMALSMNR------YIGNSI----------LPLLI 2656
Db 946 KREKLELSQRL-------SDLSEQLKQKHGEISFLNEEVKSLKQEKEQVSLRCRELEIII 998
Qy 2657 KHAYFYNEAEN-------YASLLDATL--------HTVYRLSKN----------R 2686
Db 999 NH----NRAENVQSCDTQVSSLLDGVVTMTSRGAEGSVSKVNKSFGEESKIMVEDKVSFE 1054
Qy 2687 MLTKG----QREAVSDFLVALTS-----AMQPSMLLKLLRKLTVDVSKLSEYTTVALRLL 2737
Db 1055 NMTVGEESKQEQLILDHLPSVTKESSLRATQPSENDKLQKELNVLKSEQND-----LRLQ 1109
Qy 2738 TLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCL 2797
Db 1110 MEAQRICLSLVYSTHVDQVREYMENEKDKALCSLKEELIFAQEEKIK---------- 1156
Qy 2798 IAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQPINTSSVALNND----LNTI 2852
Db 1157 ----------ELQKIHQLELQTMKTQETGDEGKPLH--LLIGKLQKAVSEECSYFLQTL 1203
Qy 2853 VQKFSEHYHDAWA----SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKE--- 2905
Db 1204 CSVLGEYYTPALKCEVNAEDKENSGDY-----ISENEDPELQDYR----YEVQDFQENMH 1254
Qy 2906 ----PVRESLKALLAI----------GWSVEHSEVDIPSNNRSSMRRQSKSGGRPPE 2948
Db 1255 TLLNKVTEEYNKLLVLQTRLSKIWGQQTDGMKLEFGEENLPKEETEFLSIHSQ------- 1307
Qy 2949 IVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQ 3008
Db 1308 ----------MTNL----------EDIDVNHKSK---------- 1321
Qy 3009 LVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYS 3068
Db 1322 ---LSSLQDLEKTKLEEQVQE----------LESLISSLQQQLKETEQNYEAEIH---- 1363
Qy 3069 LLEKLIQYIDRATINMKLLKPSTTFSRRSSFKTS----------TRDIKFFSKAVLPLME 3118
Db 1364 CLQKRLQAVSESTVPPSLPVDSVVITESDAQRTMYPGSCVKKNIDGTIEFSGE------- 1416
Qy 3119 KYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAFGPDVRITVRCL 3178
Db 1417 ----------FGVKEETNIV---KLLEKQYQEQLEEEVAKVIVSMSIAFAQQTEL----- 1458
Qy 3179 QVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTS 3238
Db 1459 ----------SRISGGKE----------NTASSKQAH---------- 1475
Qy 3239 LGYINGVLLPILTAKFDHLANCE----YGADLLLDEIQVASYKMLGSLYALGTDASLTHD 3294
Db 1476 ----------AVCQQEQHYFNEMKLSQDQI----------GFQTFETVD 1504
Qy 3295 RKYLKTEIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSL-EAQDIMQ 3353
Db 1505 VKFK----EEFKP----------LSKELGEHGKEILLSNSDPHDIPESKD--- 1540
Qy 3354 KMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSYLPFWWAQGPDNVTPTGG 3413
Db 1541 ----CVLTIS------EEMFSKDKTFIVRQSIHDEI----------SVSSMDA 1573
Qy 3414 NHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSFLPL 3473
Db 1574 SRQLMLNEEQLEDMRQ---ELVRQYQEHQQATELLRQAHMRQMERQREDQEQLQEEIKRL 1630


Qy 3474 AERVRKRT----DNMFHKEE----------SLRGFIK-------SST------DDTS 3503
Db 1631 NRQLAQRSSIDNENLVSERERVLLEELEALKQLSLAGREKLCCELRNSSTQTQNGNENQG 1690
Qy 3504 QVESQIQEDWQL----------LVRDIYS-------FYPLLIKYVDLQRNHWLRNNVPE 3545
Db 1691 EVEEQTFKEKELDRKPEDVPPEILSNERYALQKANNRLLKILLEVV--------KTTAAV 1742
Qy 3546 AEELYNHVAEIFNIWSKSQYFLKEEQNFISANEIDNMVLIMPTATRRVTAVTD-GTPQGG 3604
Db 1743 EETIGRHVLGILDRSSKSQ----SSASLIWRSEAE--ASVKSCVHEEHTRVTDESIPSYS 1796
Qy 3605 GKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGLNLFAGRE-----QEL-------VQH 3652
Db 1797 GSDMPRNDINMWSKVTEEGTELS----QRLVRSG---FAGTEIDPENEELMLNISSRLQA 1849
Qy 3653 CKDRFLKKMSEQ----DVAEFAKTQL---TLPDKIDPADEMSWQHYLYSKLGSKSKSNIT 3705
Db 1850 AVEKLLEAISETSSQLEHAKVTQTELMRESFRQKQEATESLKCQEELRERLHEESRAREQ 1909
Qy 3706 VETAENKAK-IIDDTVERIVAMSKVLFGLHMIDHPQQMSKNVYRSVVSIQRKRAVIACFR 3764
Db 1910 LAVELSKAEGVIDG-----YADEKTLFER----------QIQEKTDIIDRLE 1946
Qy 3765 QTSLHSLPRHRACNIFARTYYELWLEEENIGQEVMI----------EDLTQSFE 3808
Db 1947 QELLCASNR----------LQELEAEQQQIQEERELLSRQKEAMKAEAGPVEQQLLQETE 1996
Qy 3809 DAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLYMSYAHIIAKSCGEEEE 3868
Db 1997 KLMKEKLEVQCQAEK----------VRDDLQKQVKALEID---------- 2026
Qy 3869 EGGGEEEEGGGEAEAEDEGRASI-----HEQEMEKQ-----KLLFHQA--RLADRGVAEM 3916
Db 2027 ----VEEQVSRFIELEQEKNTELMDLRQQNQALEKQLEKMRKFLDEQAIDREHERDVFQQ 2082
Qy 3917 VLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKDKKDVGFFTSIAGLMNS 3976
Db 2083 EIQKL--------EQQLKVVPRFQPISEHQTREVEQ-LANHLKEKTD-----KCSELLLS 2128
Qy 3977 CSVLDLDAFERNTKAEGLGV---GLEGA---AGEKNMHDAEFTCALFRFIQLTCEGHNLD 4030
Db 2129 KEQLQRDIQERNEEIEKLEFRVRELEQALLVEDRKHFGAVEAKPELSLEVQLQAERDAID 2188
Qy 4031 WQNYLRTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELIDPAGKANFFKAIGVA 4090
Db 2189 RKE----------KEITNLEEQLEQF----------R 2205
Qy 4091 SQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKLSKHSSQV---DLLKE 4147
Db 2206 EELENKNEEVQQ----------LHMQLEIQKKESTTRLQELEQE 2239
Qy 4148 LLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSA 4207
Db 2240 NKLFKDDMEKLGLAIKESDAM----------STQDQHVLFGKFAQIIQEKEV---- 2281
Qy 4208 SFQEIDANNDGWVLPKDFKEKMEQQKSYTPE----------EIEFLLA---CCE 4248
Db 2282 ---EIDQLNEQ-------VTKLQQQLKITTDNKVIEEKNELIRDLETQIECLMSDQECVK 2331
Qy 4249 TNHDGKLDYIG-FCDRFHEPAKEIGFNLAVLLTNLSEH----------MPNEPRLARFL 4296
Db 2332 RNREEEIEQLNEVIEKLQQELANIGQKTSMNAHSLSEEADSLKHQLDVVIAEKLALEQQV 2391
Qy 4297 ETAGSVLNYFEPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKPQ-IKESKRAFFYSIVT 4355
Db 2392 ETANEEMTFMKNVLKETNFK--MNQLTQELFSLKRER-ESVEKIQSIPENS----VNVAI 2444
Qy 4356 EGGDKEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKD 4415
Db 2445 DHLSKDKPELEVVLTEDALKSLENQTYFKSFEENGKGSIINLETRLLQL---ESTVSAKD 2501
Qy 4416 -PFRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGV 4474

```
Db       2502 LELTQCYKQIKD--MQEQGQFETEMLQKKIVNLQKIVEEKVAAALVSQI---------QL 2550

Qy       4475 LVVVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQ 4534

Db       2551 EAVQEY-----AKFCQDNQTISSEPERTNIQNLNQLRE----------------DELGS 2588

Qy       4535 MQVSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLL 4594

Db       2589 -DISALTLRISELESQVVEM------HTSLILEKEQVEIAEKNVLE--KEKKLLELQKLL 2639

Qy       4595 GGEQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQG--------PAPSALSQVDLSQYTR 4646

Db       2640 EGNEKKQREKEKKRSPQDVEVLKTTTELFHSNEESGFFNELEALRAESVATKAELASYKE 2699

Qy       4647 RA 4648

Db       2700 KA 2701


RESULT 5
US-11-090-997-876
; Sequence 876, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
;  APPLICANT: Betsholtz, Christer et. al.
;  TITLE OF INVENTION: Glomerular Expression Profiling
;  FILE REFERENCE: 04-1059
;  CURRENT APPLICATION NUMBER: US/11/090,997
;  CURRENT FILING DATE:  2005-03-25
;  NUMBER OF SEQ ID NOS: 2985
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 876
;   LENGTH: 3842
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-090-997-876

  Query Match             1.1%;  Score 301.5;  DB 7;  Length 3842;
  Best Local Similarity   17.9%;  Pred. No. 9.8e-09;
  Matches  592;  Conservative  458;  Mismatches 1161;  Indels 1089;  Gaps  140;

Qy       1800 AAHALCTHVDQKQL--LYAIQSQYM--------------SGPL---RQGFYDLLIALHL 1839

Db         48 AHHDL--NIDQSQCNEMYINSSQRVESTVIPESTIMRTLHSGEITSHEQGF-----SVEL 100

Qy       1840 ESH-ATTMEACKNE-----FVIPLGPELKALYEEP---DMGHSLRSLQTESVRPQMKMTD 1890

Db        101 ESEISTTADDCSSEVNGCSFVMRTGKPTNLLREEEFGVDDSYSEQGAQDSPTHLEMMESE 160

Qy       1891 IAESITEISNLYSPYFPLEVA---------REF-----------------VMQALAEAVE 1924

Db        161 LAGKQHEIEELNRELEEMRVTYGTEGLQQLQEFEAAIKQRDGIITQLTANLQQARREKDE 220

Qy       1925 T-----------------NQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKL 1966

Db        221 TMREFLELTEQSQKLQIQFQQLQASETLRNSTHSSTAADLLQAKQQILTHQQQLEEQDHL 280

Qy       1967 L---------------IMTNPETWDPSFDKEGKDEHRKGL---------LHMKMAEGAK 2001

Db        281 LEDYQKKKEDFTMQISFLQEKIKVYEMEQDKKVENSNKEEIQEKETIIEELNTKIIEEEK 340

Qy       2002 LQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTRE 2061

Db        341 ----------KTLELKDK----LTTADKLLGELQEQIVQKNQEIKNMKLELTNSKQKERQ 386

Qy       2062 FRCPPREQMNAILSF---------------KHLEEEDKENCPCGEELIARMNEFHDTLMA 2106

Db        387 SSEEIKQLMGTVEELQKRNHKDSQFETDIVQRMEQETQRKL---EQLRAELDEMYGQQIV 443

Qy       2107 HVSLHALQEPDAAENQEPEAKPGAFGKLYNII-------------------------- 2138

Db        444 QMKQELIRQHMA---QMEEMKTRHKGEMENALRSYSNITVNEDQIKLMNVAINELNIKLQ 500
```

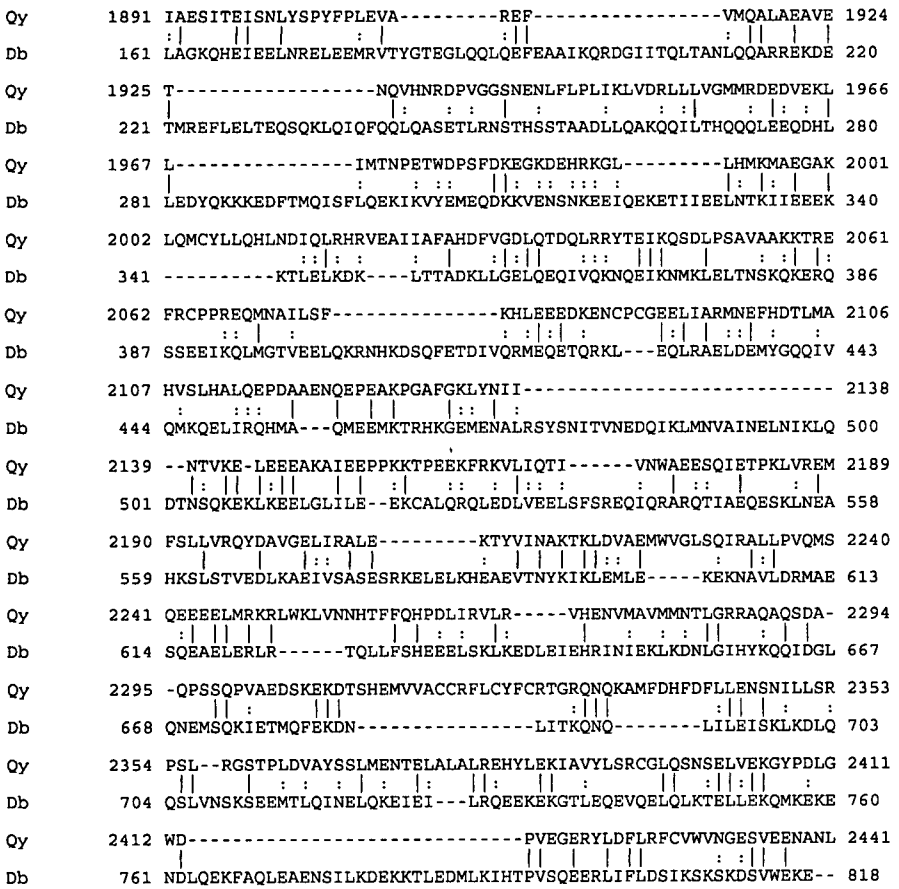
```
Qy       2139 --NTVKE-LEEEAKAIEEPPKKTPEEKFRKVLIQTI------VNWAEESQIETPKLVREM 2189

Db        501 DTNSQKEKLKEELGLILE--EKCALQRQLEDLVEELSFSREQIQRARQTIAEQESKLNEA 558

Qy       2190 FSLLVRQYDAVGELIRALE---------KTYVINAKTKLDVAEMWVGLSQIRALLPVQMS 2240

Db        559 HKSLSTVEDLKAEIVSASESRKELELKHEAEVTNYKIKLEMLE-----KEKNAVLDRMAE 613

Qy       2241 QEEEELMRKRLWKLVNNHTFFQHPDLIRVLR-----VHENVMAVMMNTLGRRAQAQSDA- 2294

Db        614 SQEAELERLR------TQLLFSHEEELSKLKEDLEIEHRINIEKLKDNLGIHYKQQIDGL 667

Qy       2295 -QPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSR 2353

Db        668 QNEMSQKIETMQFEKDN----------------LITKQNQ--------LILEISKLKDLQ 703

Qy       2354 PSL--RGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLG 2411

Db        704 QSLVNSKSEEMTLQINELQKEIEI---LRQEEKEKGTLEQEVQELQLKTELLEKQMKEKE 760

Qy       2412 WD-----------------------------PVEGERYLDFLRFCVWVNGESVEENANL 2441

Db        761 NDLQEKFAQLEAENSILKDEKKTLEDMLKIHTPVSQEERLIFLDSIKSKSKDSVWEKE-- 818

Qy       2442 VIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPE 2501

Db        819 -IEILIE-----------ENEDLKQQCIQLNEEIEK--QRNTFSFAEKNFEVNY------ 858

Qy       2502 SDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKN-ESLRARAILRSLVPLEDLQ 2560

Db        859 QELQEEY----ACLLKVKDDLED-------------SKNKQELEYKSKLKALNEELHLQ 900

Qy       2561 GVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLE--RVYGIETQELFYKLLEEA 2618

Db        901 RI--------NPTTVK------MKSSVFDEDKTFVAETLEMGEVVEKDTTELMEK-LEVT 945

Qy       2619 FLPDLRAATMLDRNDGCESDMALSMNR------YIGNSI---------------LPLLI 2656

Db        946 KREKLELSQRL-------SDLSEQLKQKHGEISFLNEEVKSLKQEKEQVSLRCRELEIII 998

Qy       2657 KHAYFYNEAEN-------YASLLDATL--------HTVYRLSKN--------------R 2686

Db        999 NH----NRAENVQSCDTQVSSLLDGVVTMTSRGAEGSVSKVNKSFGEESKIMVEDKVSFE 1054

Qy       2687 MLTKG----QREAVSDFLVALTS-----AMQPSMLLKLLRKLTVDVSKLSEYTTVALRLL 2737

Db       1055 NMTVGEESKQEQLILDHLPSVTKESSLRATQPSENDKLQKELNVLKSEQND-----LRLQ 1109

Qy       2738 TLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCL 2797

Db       1110 MEAQRICLSLVYSTHVDQVREYMENEKDKALCSLKEELIFAQEEKIK------------ 1156

Qy       2798 IAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQPINTSSVALNND----LNTI 2852

Db       1157 ----------ELQKIHQLELQTMKTQETGDEGKPLH--LLIGKLQKAVSEECSYFLQTL 1203

Qy       2853 VQKFSEHYHDAWA----SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKE--- 2905

Db       1204 CSVLGEYYTPALKCEVNAEDKENSGDY-----ISENEDPELQDYR----YEVQDFQENMH 1254

Qy       2906 ----PVRESLKALLAI-------------GWSVEHSEVDIPSNNRSSMRRQSKSGGRPPE 2948

Db       1255 TLLNKVTEEYNKLLVLQTRLSKIWGQQTDGMKLEFGEENLPKEETEFLSIHSQ------- 1307

Qy       2949 IVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVTNGGGIHPQ 3008

Db       1308 ----------------MTNL----------------EDIDVNHKSK------------ 1321

Qy       3009 LVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQTTTGVAIELRFAYS 3068

Db       1322 ---LSSLQDLEKTKLEEQVQE----------LESLISSLQQQLKETEQNYEAEIH---- 1363
```

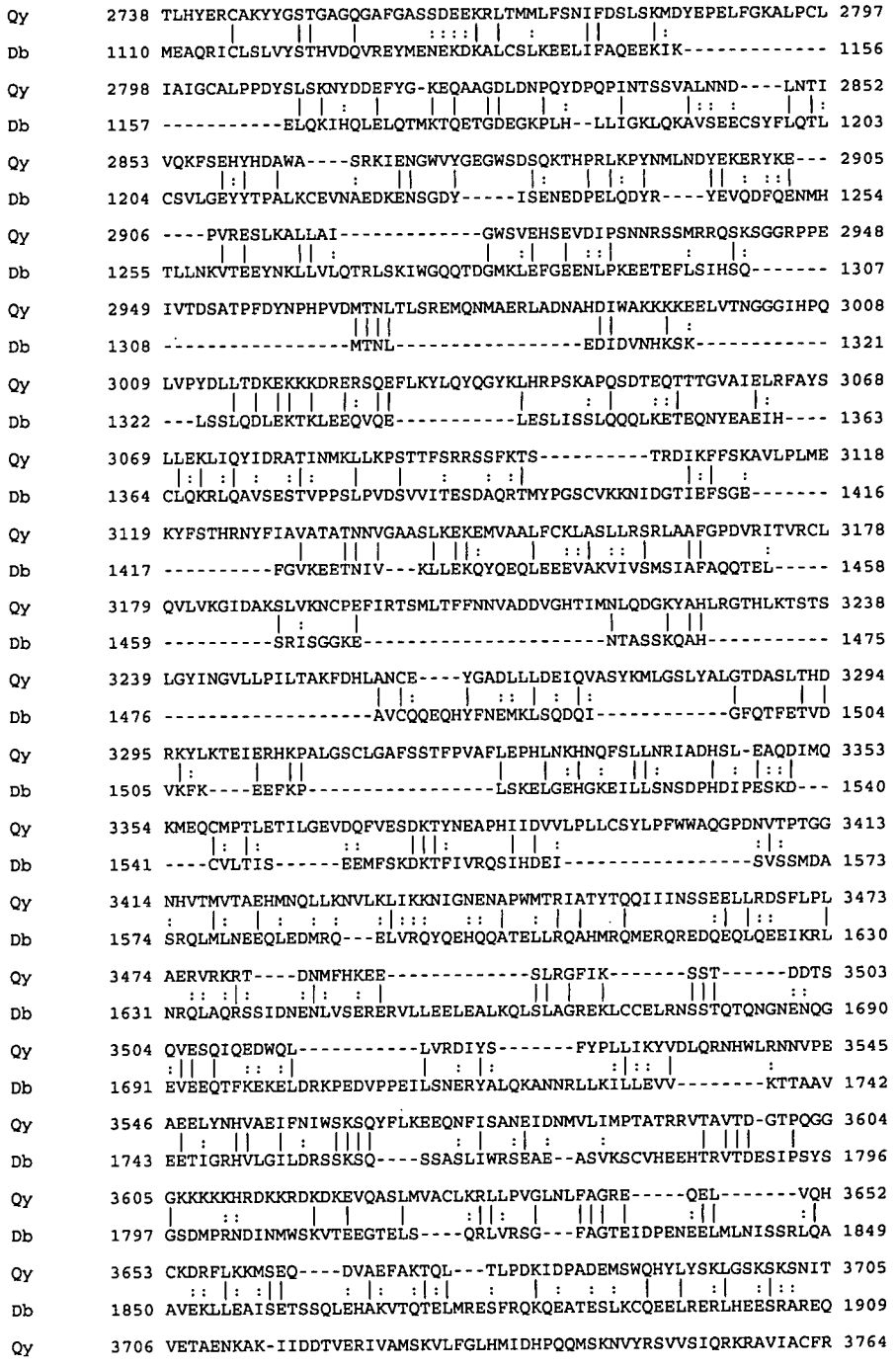


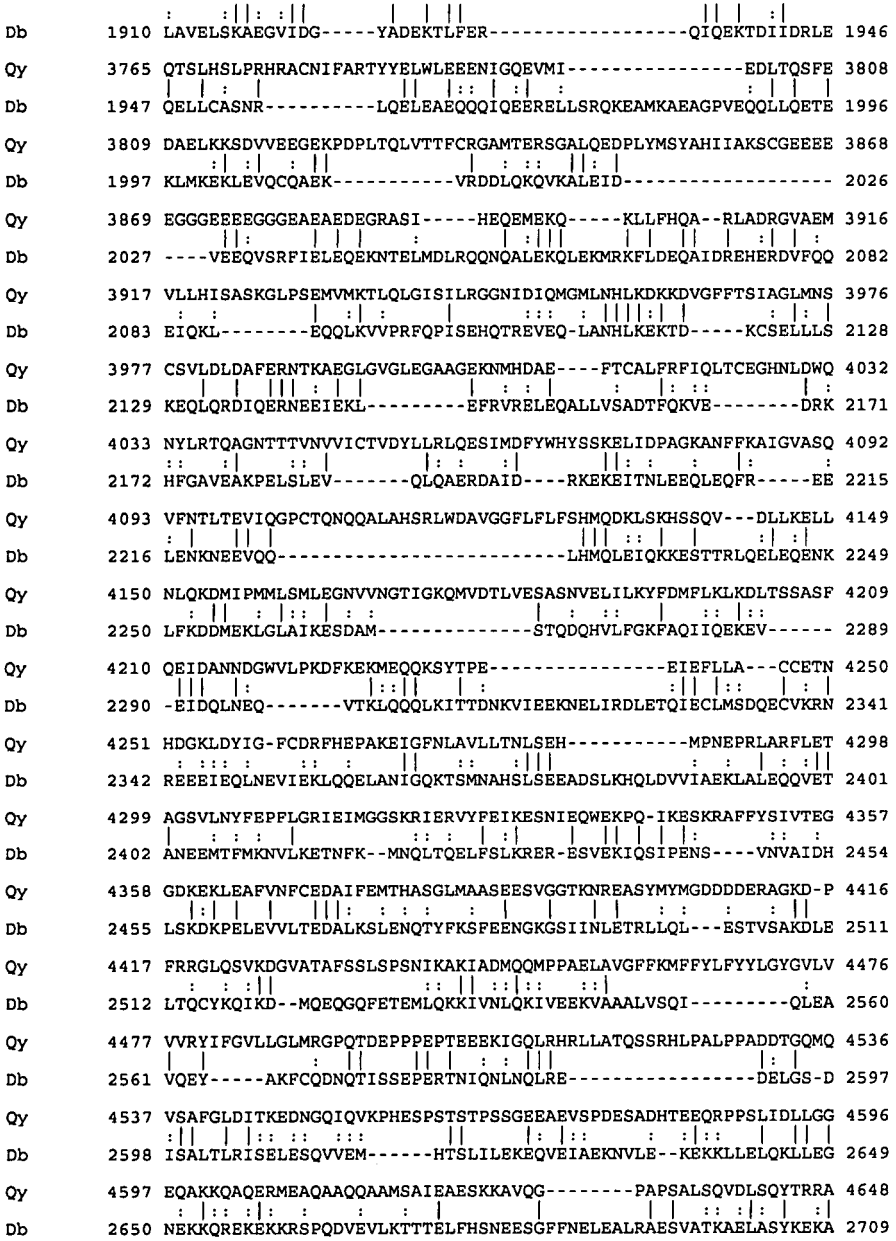


RESULT 6
US-11-090-997-872
; Sequence 872, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 872
; LENGTH: 3896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-872

Query Match 1.1%; Score 301.5; DB 7; Length 3896;
Best Local Similarity 17.9%; Pred. No. 1e-08;
Matches 592; Conservative 458; Mismatches 1161; Indels 1089; Gaps 140;

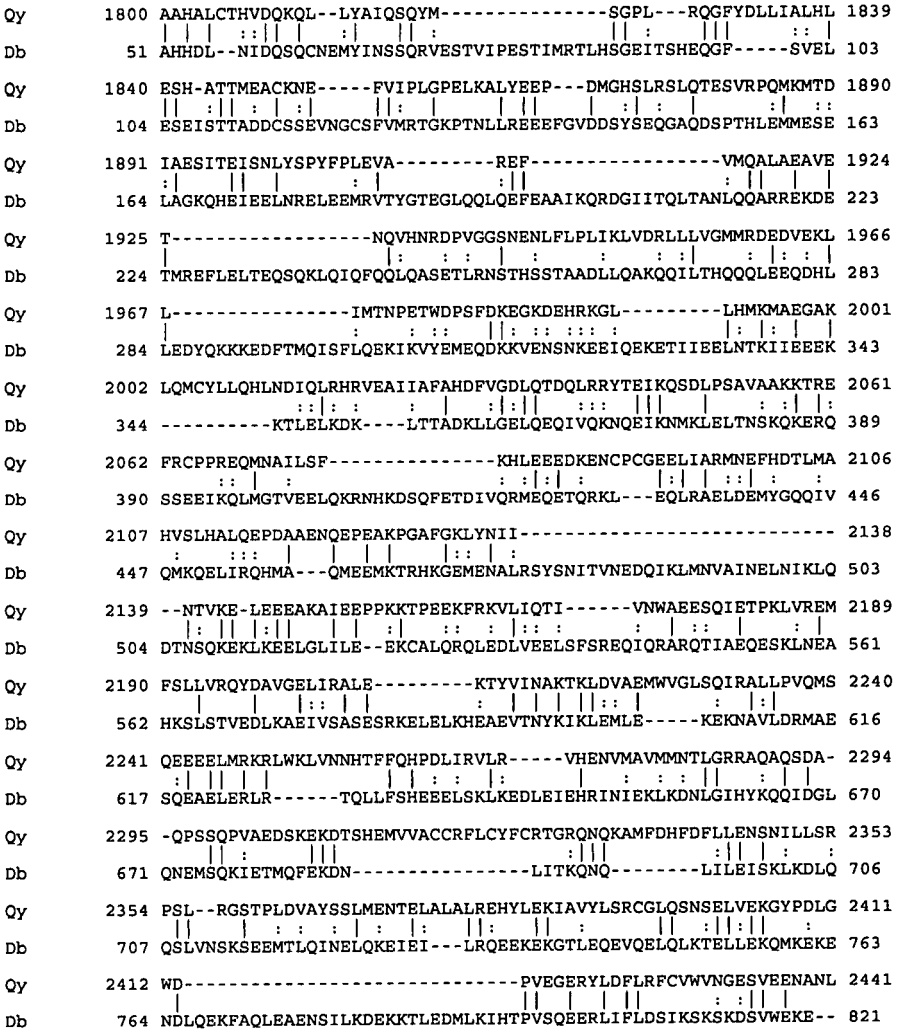




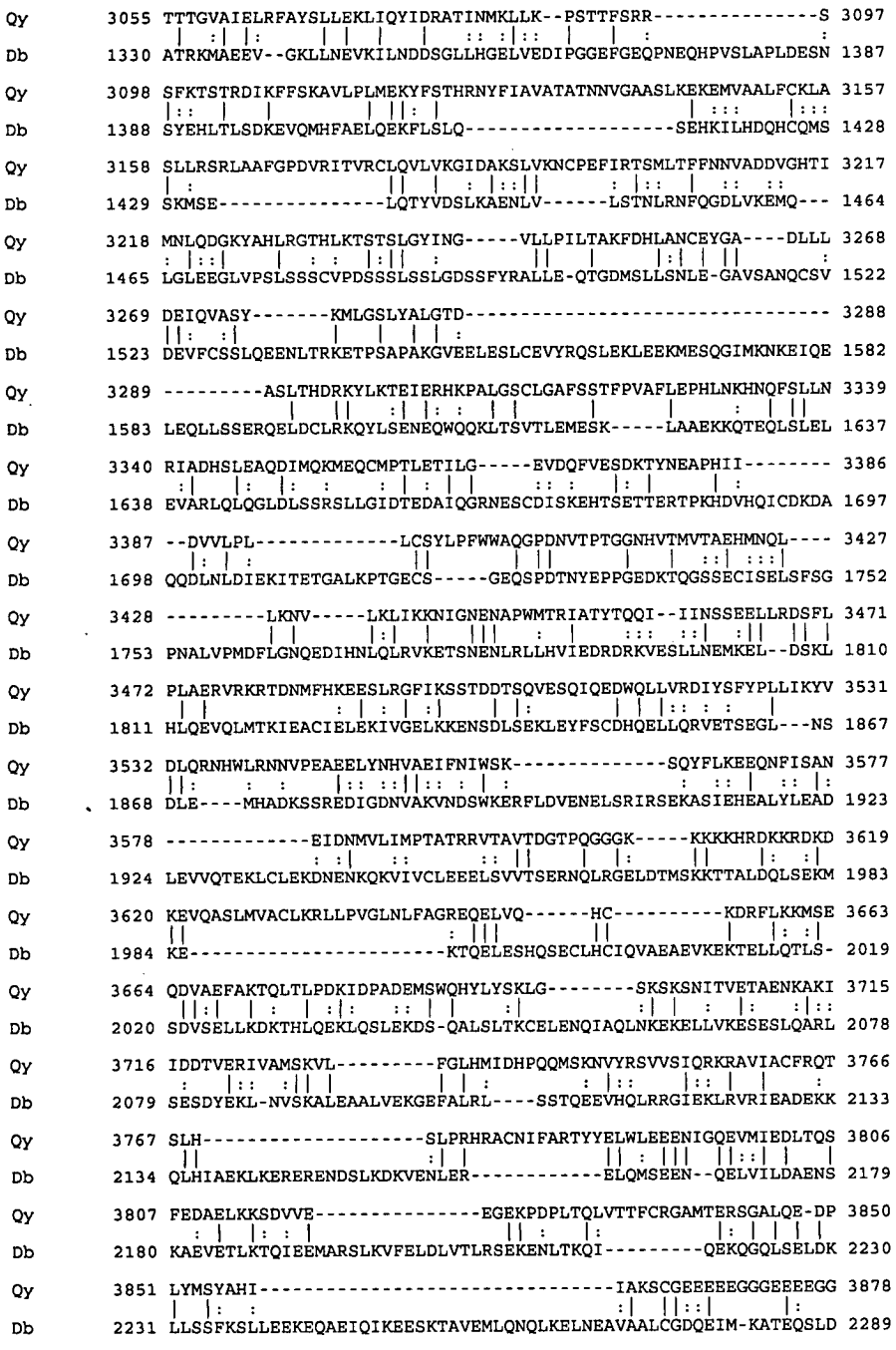


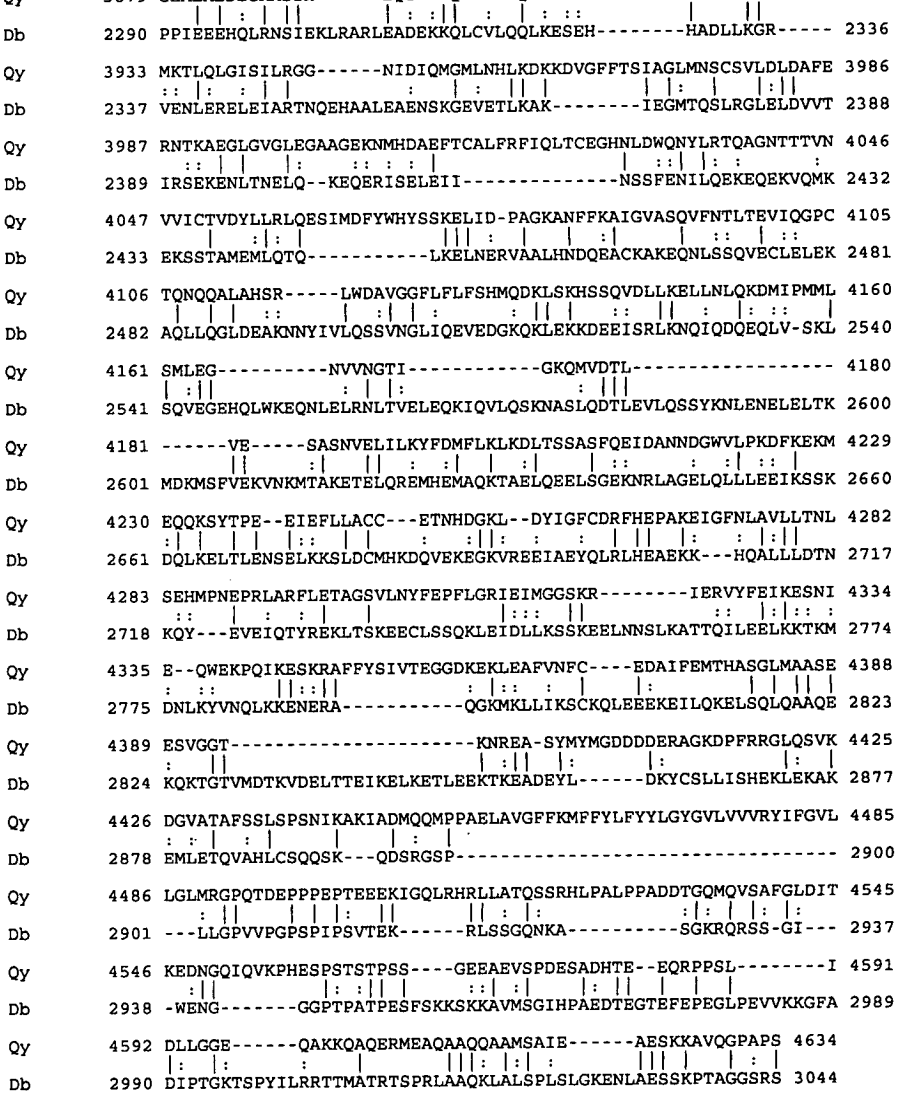
RESULT 7
US-11-090-997-868
; Sequence 868, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 868
; LENGTH: 3907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-868

Query Match 1.1%; Score 301.5; DB 7; Length 3907;
Best Local Similarity 17.9%; Pred. No. 1e-08;
Matches 592; Conservative 458; Mismatches 1161; Indels 1089; Gaps 140;



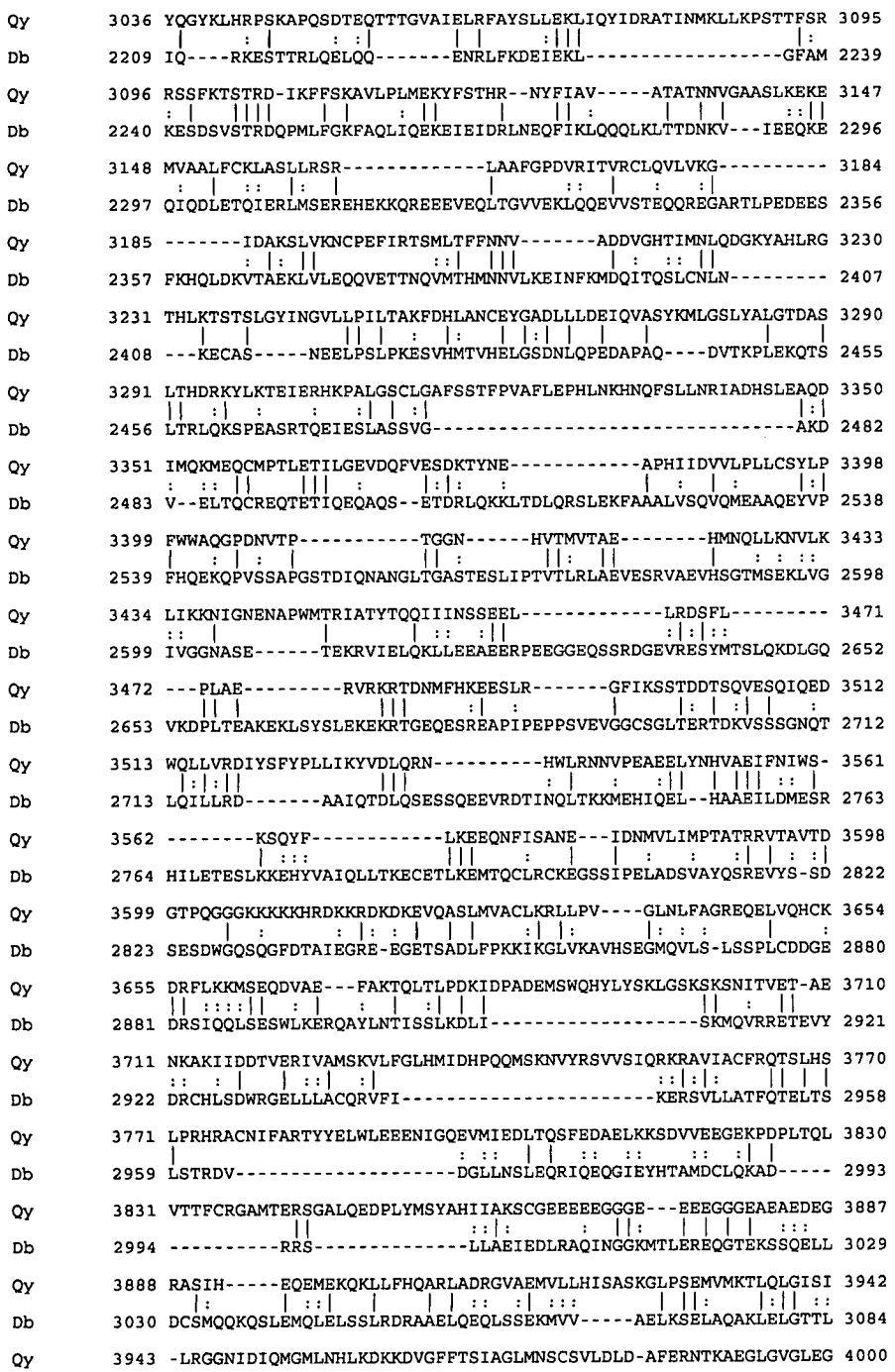
```
Db       2458 LSKDKPELEVVLTEDALKSLENQTYFKSFEENGKGSIINLETRLLQL---ESTVSAKDLE 2514

Qy       4417 FRRGLQSVKDGVATAFSSLSPSNIKAKIADMQQMPPAELAVGFFKMFFYLFYYLGYGVLV 4476

Db       2515 LTQCYKQIKD--MQEQGQFETEMLQKKIVNLQKIVEEKVAAALVSQI---------QLEA 2563

Qy       4477 VVRYIFGVLLGLMRGPQTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGQMQ 4536

Db       2564 VQEY-----AKFCQDNQTISSEPERTNIQNLNQLRE----------------DELGS-D 2600

Qy       4537 VSAFGLDITKEDNGQIQVKPHESPSTSTPSSGEEAEVSPDESADHTEEQRPPSLIDLLGG 4596

Db       2601 ISALTLRISELESQVVEM------HTSLILEKEQVEIAEKNVLE--KEKKLLELQKLLEG 2652

Qy       4597 EQAKKQAQERMEAQAAQQAAMSAIEAESKKAVQG--------PAPSALSQVDLSQYTRRA 4648

Db       2653 NEKKQREKEKKRSPQDVEVLKTTTELFHSNEESGFFNELEALRAESVATKAELASYKEKA 2712


RESULT 8
US-10-505-928-325
; Sequence 325, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 325
;   LENGTH: 3113
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-325

  Query Match             1.1%;  Score 283;  DB 6;  Length 3113;
  Best Local Similarity   18.0%;  Pred. No. 9.5e-08;
  Matches  636;  Conservative  474;  Mismatches 1205;  Indels 1220;  Gaps  148;

Qy       1762 EEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQY 1821

Db         68 ENQRLMEICESLEKTK-------------------QKISHEL--QVKESQV------NF 99

Qy       1822 MSGPLRQGFYDLLIALHLESHATTMEACKNE-----------------------FVIPL 1857

Db        100 QEGQLNSG------KKQIEKLEQELKRCKSELERSQQAAQSADVSLNPCNTPQKIFTTPL 153

Qy       1858 GP----------ELKALY-----EEPDMGHSLRSLQTESVR---PQMKMT--DIA--ESI 1895

Db        154 TPSQYYSGSKYEDLKEKYNKEVEERKRLEAEVKALQAKKASQTLPQATMNHRDIARHQAS 213

Qy       1896 TEI---------SNLYSPYFPLEVAREFVM------QALAEAVETNQVHNRDPVGGSNEN 1940

Db        214 SSVFSWQQEKTPSHLSSNSQRTPIRRDFSASYFSGEQEVTPSRSTLQIGKRDANSSFFDN 273

Qy       1941 LFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGA 2000

Db        274 SSSP--HLLDQL---------------------------------------------- 283

Qy       2001 KLQMCYLLQHLNDIQLR---HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAK 2057

Db        284 KAQNQELRNKINELELRLQGHEKE-------------MKGQVNKFQEL-QLQLEKAKV-- 327

Qy       2058 KTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPD 2117

Db        328 --------------------ELIEKEKVLNKCRDELVRTTAQYDQASTKYTAL------- 360

Qy       2118 AAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVL---------- 2167

Db        361 -----EQKLK-----KLTEDLSCQRQNAESARCSLEQKIKEKEKEFQEELSRQQRSFQTL 410

Qy       2168 ----IQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAE 2223

Db        411 DQECIQMKARLTQELQ-----QAKNMHNVLQAELDKLTSVKQQLENN-LEEFKQKLCRAE 464

Qy       2224 MWVGLSQIRALLPVQMSQEEEELMRK-RLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMN 2282

Db        465 QAFQASQIK----------ENELRRSMEEMKKENN----------LLKSHSEQKAREVC 503

Qy       2283 TLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDF 2342

Db        504 HLEAELKNIKQCLNQSQNFAEEMKAKNTSQETML------------RDLQEKINQQ--- 547

Qy       2343 LLENSNILLSRPSLRGSTPLDVAYSSLMENTELA---LALREHYLEKIAVYLSRCGLQSN 2399

Db        548 --ENSLTL---------EKLKLAVADLEKQRDCSQDLLKKREHHIEQLNDKLSKTEKESK 596

Qy       2400 S-----ELVEKGYPDLGWDPVEGERYLDFLRFCVW--------VNGESVEENA------- 2439

Db        597 ALLSALELKKKEY------ELKEEKTL----FSCWKSENEKLLTQMESEKENLQSKINHL 646

Qy       2440 --------------NLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLR 2485

Db        647 ETCLKTQQIKSHEYNERVRTLEMDRENLSVEIRN-----LHNVLDSKSVE---VETQKLA 698

Qy       2486 EMEQEGDVNFS-------------------------HPL-----PESDEDEDYIDTGAA 2514

Db        699 YMELQQKAEFSDQKHQKEIENMCLKTSQLTGQVEDLEHKLQLLSNEIMDKDRCYQDLHAE 758

Qy       2515 ILNFYCTLVDLLGRCAPDAGVIA---------------------------------- 2537

Db        759 ----YESLRDLLK--SKDASLVTNEDHQRSLLAFDQQPAMHHSFANIIGEQGSMPSERSE 812

Qy       2538 --LGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSV 2595

Db        813 CRLEADQSPKNSAILQNRVD--------SLEFSLES----QKQMNSDL-------QKQCE 853

Qy       2596 GLF---------------LERVYGIETQELFYKLLEEAFLPDLRAATMLDR--------- 2631

Db        854 ELVQIKGEIEENLMKAEQMHQSFVAETSQRISKLQEDTSAHQNVVAETLSALENKEKELQ 913

Qy       2632 --NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLT 2689

Db        914 LLNDKVETEQAEIQELKKSNHLLEDSLKELQLLSET---LSLEKKEMSSIISLNKREIEE 970

Qy       2690 KGQREAVSDFLVALTSAMQPSMLLK------LLRKLTVDVSKLS-EYTTVALRLLTLHYE 2742

Db        971 LTQENGTLKEINASLNQEKMNLIQKSESFANYIDEREKSISELSDQYKQEKLILL----Q 1026

Qy       2743 RCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSL-----SKMDYEPELFGKA-LPC 2796

Db       1027 RCEETGNAYEDLSQKYKAAQEKNSKLECLL--NECTSLCENRKNELEQLKEAFAKEHQEF 1084

Qy       2797 LIAIGCALPPDYSL----------SKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVA 2844

Db       1085 LTKLAFAEERNQNLMLELETVQQALRSEMTDNQNNSKSEAGG----LKQEIMTLKEEQNK 1140

Qy       2845 LNNDLNTIVQK----------------FSEHYHDAWASRKIENGWVYGEGWSDSQKTHP 2887

Db       1141 MQKEVNDLLQENEQLMKVMKTKHECQNLESEPIRNSVKERESERNQCNFKPQMDLEVKEI 1200

Qy       2888 RLKPYN--------MLND-----YEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRS 2934

Db       1201 SLDSYNAQLVQLEAMLRNKELKLQESEKEKECLQHELQTIRG----------DLETSNLQ 1250

Qy       2935 SMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKK 2994

Db       1251 DMQSQEISGLKDCEI--DAEEKYISGPHELSTS--------QN------DNAH------- 1287

Qy       2995 KEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQYQGYKLHRPSKAPQSDTEQ 3054

Db       1288 --------------LQCSLQTTMNKLNELEKICEI---LQAEKYELVTELNDSRSECIT 1329
```





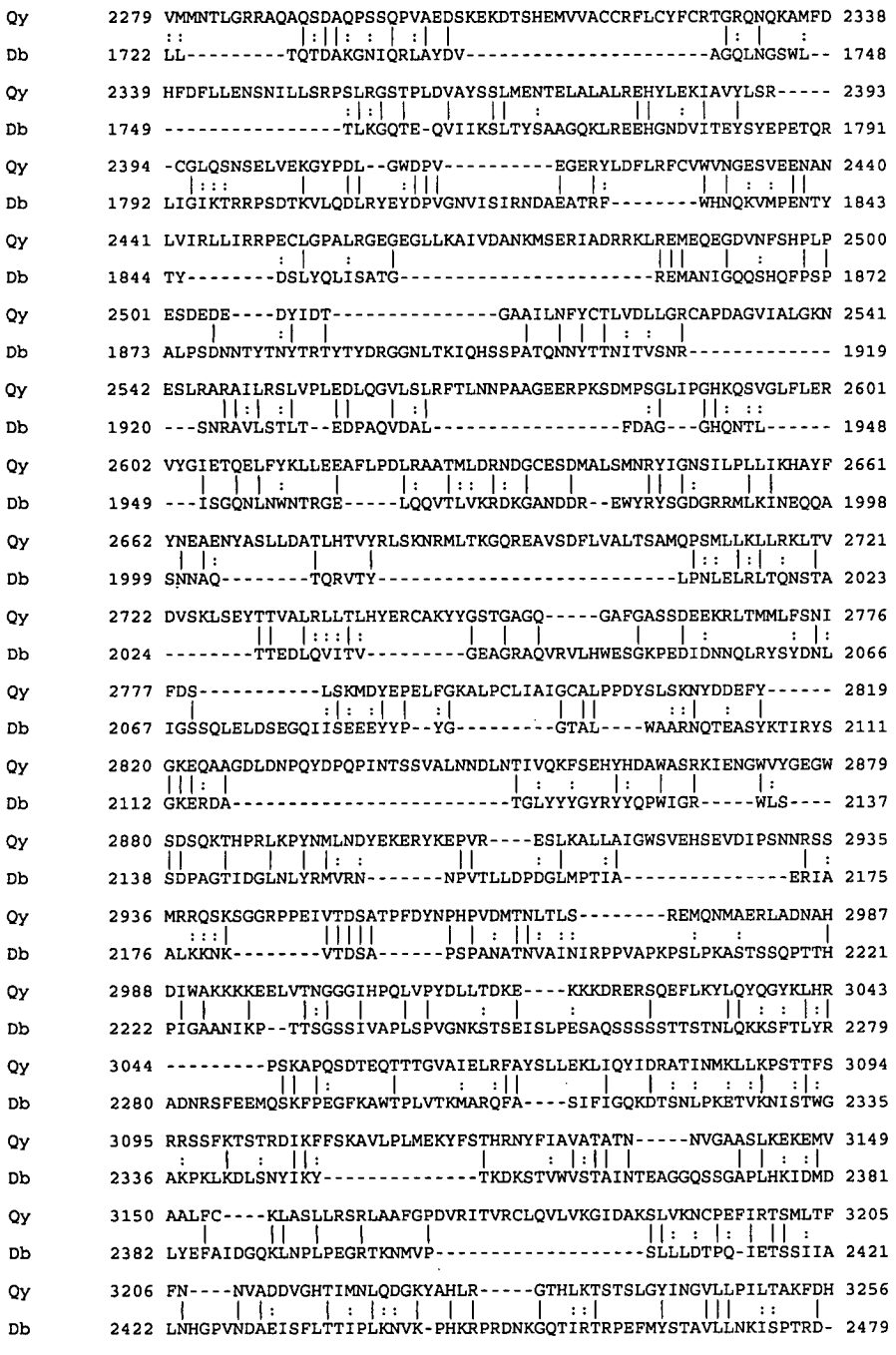
RESULT 9
US-11-090-997-10
; Sequence 10, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3

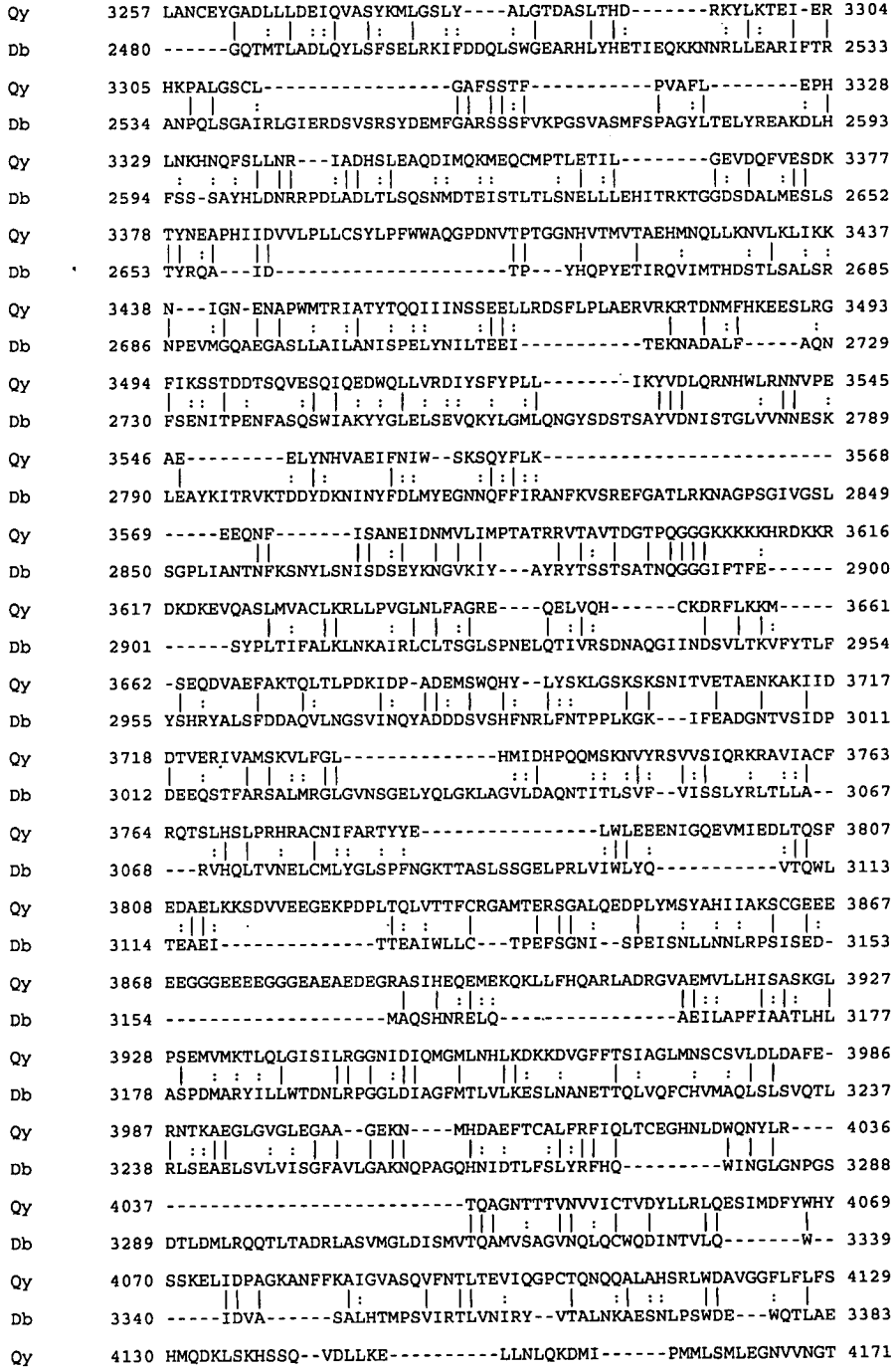
```
; SEQ ID NO 10
;   LENGTH: 3811
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-090-997-10

  Query Match             0.9%;  Score 253.5;  DB 7;  Length 3811;
  Best Local Similarity   17.0%;  Pred. No. 9.6e-06;
  Matches  660;  Conservative  560;  Mismatches 1411;  Indels 1245;  Gaps  157;

Qy       1249 QPIFENTDEMIDTRIDVT-------RIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLP 1301
Db        542 QTIAEQENRLSEARKSLSTVEDLKAEIVAASESRKELELKHEAEITNYKIKLEMLEKE-- 599

Qy       1302 VICHNEFID--------EAEKARRWVEIKDRQQI-LMKEAVEAQMPAHIDQIMRSGFTMN 1352
Db        600 ---KNAVLDRMAESQEAELERLRTQLLFSHEEELSKLKEDLEVEHRINIEK-------LK 649

Qy       1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQN--------YNNLQPGQVNG- 1403
Db        650 DNLGIHYKQQIDGLQNEMNRKMESMQCETDNL---ITQQNQLILENSKLRDLQECLVNSK 706

Qy       1404 -------MHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKS 1456
Db        707 SEEMNLQINELQKEIEILKQEEKEKGTLEQEVQE---------LQLKTEQLEKQLKEKED 757

Qy       1457 KTPDPFS--DTEVSPERGARRP-NPQIKV-SQANQRYNGMNARPSRTNLYGSQVGLNMA- 1511
Db        758 DLQEKCAQLDAENNILKEEKRVLEDKLKMYSPSEQEERSIAVDPSTSKSADSRWQKEVAM 817

Qy       1512 --TPTQDRKQ----MTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVY 1565
Db        818 LRKETEDLQQQCLYLNEEIEKQRNTFAFAEKNFEVNYQELQREYTCLLKI---------- 867

Qy       1566 IGWVTTQYHLHSKDFNQSKVTKSSVIITDDYD---RVVENVNRQSCYMVRADELYNEVMA 1622
Db        868 ------------RDDLEATQTKQAL----EYESKLRALE------------EELLSKRGN 899

Qy       1623 EATAKGASQGMF------IGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEAT 1676
Db        900 PAAPKGKSSGIFPSETLEIGEVVEKDTTEL---MEKLEVTKREKLELSEK------VSGL 950

Qy       1677 SKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWAR---------- 1726
Db        951 SEQLKQTH----CTINSLSAEV------RALKQEKEQLLLRCGELELLANPSGTENAAVC 1000

Qy       1727 -VPNQSLQVHAL--KLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHS 1783
Db        1001 PVQMSSYQAGLVMGKVGDSGG-------SISKISKDLAEESK------PMIEDKIPFKES 1047

Qy       1784 HTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHA 1843
Db        1048 GREQLLLPTRAQKPSHATVEPCESEKLQQELHALKAEQDDLRLQMEAQRICLFVVYSTHA 1107

Qy       1844 TTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYS 1903
Db        1108 DQVRA----------------HMEKEREEALCSLKDELISAQQKKID------ELHKMHQ 1145

Qy       1904 PYF-----------PLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRL 1952
Db        1146 CQLQNFKIQETGDEPLQVLIERLQQAVSEKC----FHISKTLNNVFDECYTP-------- 1193

Qy       1953 LLVGMMRDEDVEKLLIMT----NPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLL 2008
Db        1194 -LKCEMNIEEKENSGVYTSQNQSPELQEYRYEVQDFQESMQVLLGKVTEECRKLS--GLQ 1250

Qy       2009 QHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR-------RYTEIK-QSDLPSAVAAKKTR 2060
Db        1251 TRLGKIHEQQTDGVALEFAEQNAAEEEAGLLSGCSQSALQSTDVSLESKVSSLPASEKSR 1310

Qy       2061 EFRCPPREQMNAILSFK-HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAA 2119
Db        1311 ECERQVQELQSPVAAGQLQLTETEANHRAETESLQQRLEAVSE---------APVQPSLS 1361

Qy       2120 ENQEPEAKPGAFGKLY-------NIINTVK-----ELEEEAKAI---EEPPKKTPEEKFR 2164
Db        1362 IDSVVFKGSGAQKPVYCGSCLRECVDGTAKFSDRFEVRQETNMVNLMEKQYQERLEEEIA 1421

Qy       2165 KVLIQTIVNWAEESQIE----------------------------------------T 2182
Db        1422 KVIVSMSIAFAQQTELSRLSEGKENTIQSEQAHTLCSQNKHQLNDITSQSQVGLQTFEAT 1481

Qy       2183 PKLVREMFSLLVRQ------------YD-------------AVGELIRALEKTYVINAKT 2217
Db        1482 DKNFKEEFKPLSKELGEYRKAVPLSSHDDLDDILKSEEHGLAISEEIFSKDETFIVRKSM 1541

Qy       2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277
Db        1542 HDEVLVSSMDTSR-QLILNEQLEDMRQELVRQ----------YEEHQQATEMLR------ 1584

Qy       2278 AVMMNTLGRRAQAQSDAQPSSQPVAEDSKEK---DTSH----------------EMVVA 2317
Db        1585 QAHMQQMERQREDQEQLQEEIKRLNEQLAQKSSIDTEHVVSERERVLLEELEALKQLPLA 1644

Qy       2318 CCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELAL 2377
Db        1645 GRKELC--CELRHSSTQTQDGHDDQEVEEQTL---KDKTLERSPEDALLDRNLSNERYAL 1699

Qy       2378 ALREHYLEKIAVYLSR------------CGL-------QSNSELVEKGYPDLG---WDP 2414
Db        1700 KKANNRLLKILLEVVKTTSAAEETIGRHVLGILDRSSKGQTASSLLWRSEADASATTCAP 1759

Qy       2415 VEGERYLD-----------FLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGEGEG 2463
Db        1760 EDCARAMDESIPSYPGTAIATHDSIW--SKVTEEGAELSQRLV--RSGFAGPVIDPENEE 1815

Qy       2464 LLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDE--DEDYIDTGAAILNFYCT 2521
Db        1816 LM-----LNISSRLQAAVEKLLEAISETNTQLEHAKVTQTELMRESFRQKQEATESLHC- 1869

Qy       2522 LVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKS 2581
Db        1870 LEELRERL-----------QEESRAREQL----------------------AEELNKA 1894

Qy       2582 DMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMAL 2641
Db        1895 E---SVIDGYSDEKTLFERQIQ--EKTDIIEHLEQEVL-------CMNNRLQELESDQR- 1941

Qy       2642 SMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAV----- 2696
Db        1942 ------------------------------------RVEEERQLLCRQREAMRAEAG 1962

Qy       2697 ---SDFLVALTSAMQPSM-----------LLKLLRKLTVDVSKLSEYTTVALRLLTLHY 2741
Db        1963 PVEQQFLQETEKLMKEKLEVQCQAEKVRGDLQKQVKALEIDVEE------QVSRFIELEQ 2016

Qy       2742 ERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIG 2801
Db        2017 EKNAELTDLRQQSQAL-------EKQLEKM---------------------------- 2039

Qy       2802 CALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYH 2861
Db        2040 ----------RKFLDE-----------------QAID----------------REHER 2054

Qy       2862 DAWAS--RKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGW 2919
Db        2055 DVFQQEIQKLEH----------QLKAVPRIQPVSEHQARFVEQLTNHLKEKTDRCSELLL 2104

Qy       2920 SVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPF----DYNPHPVDMTNLTLSREM 2975
Db        2105 SKEQLQRDIQERNEEIEKLECRVRELEQALLA-SAEPFPKVEDQKRSGAVEADPELSLEV 2163

Qy       2976 QNMAERLADNAHDIWAKKKKEELVTNGGGIHPQLVPYDLLTDKEKKKDRERSQEFLKYLQ 3035
Db        2164 QLQVER------DATDRKQKE--ITN---LEEQLEQF----REELENKNDEVQELLMQLE 2208
```



RESULT 10
US-11-070-573-68
; Sequence 68, Application US/11070573
; Publication No. US20060168683A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Cai, Charles
; APPLICANT: Meade, Thomas
; APPLICANT: Moon, Haley
; APPLICANT: Burton, Stephanie
; APPLICANT: Sheets, Joel
; APPLICANT: Merlo, Donald
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins
; FILE REFERENCE: DAS-118XC1
; CURRENT APPLICATION NUMBER: US/11/070,573
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/549,502
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: 60/549,516
; PRIOR FILING DATE: 2004-03-02

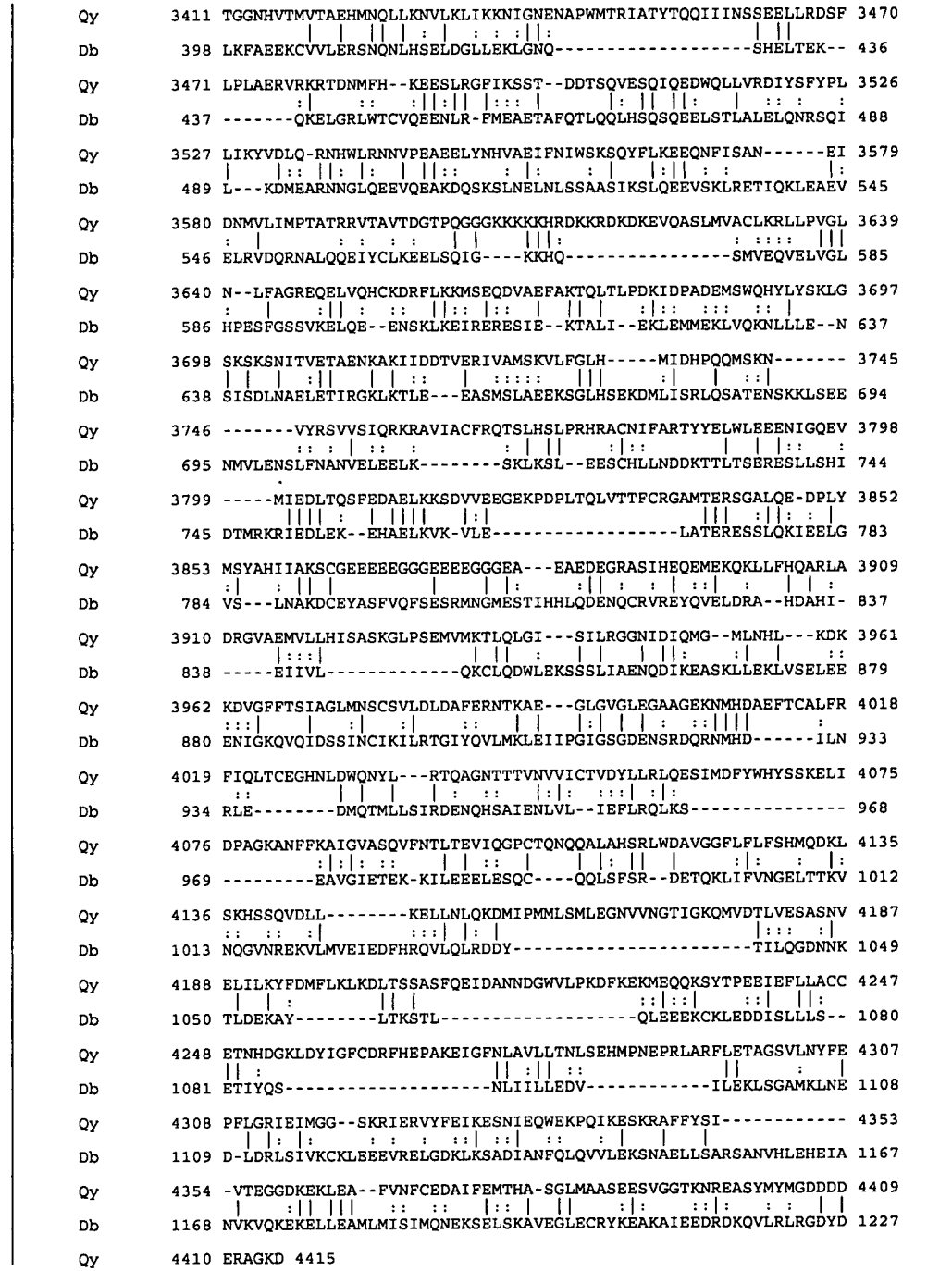
```
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 5001
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of the 8836 "BCA" triple fusion protein
;   OTHER INFORMATION: encoded by SEQ ID NO:67
US-11-070-573-68

  Query Match            0.8%;  Score 224.5;  DB 7;  Length 5001;
  Best Local Similarity  17.7%;  Pred. No. 0.001;
  Matches  781;  Conservative  545;  Mismatches 1508;  Indels 1583;  Gaps  216;

Qy    695 GYVP-----YPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDV 749
Db     50 GYAPAFTLNY--------NSGAGNSPFGLG------WDCNVMTIRRRTHFGVPHYDETDT 95

Qy    750 -IGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRY 808
Db     96 FLGPEGEVLV-----VADQPRDESTLQGINL-GATFTVTGYRSRLESHF------SRLEY 143

Qy    809 AAPE--------------------GYSPLVESLLPQQILSLEPCFYFGNLSKRALAGPPL 848
Db    144 WQPKTTGKTDFWLIYSPDGQVHLLGKSPQARISNPSQTTQTAQWLLEASVSSR---GEQI 200

Qy    849 -----VQDDTAFVPTPV-DTLQITLPTYVEQI---RDKLAENIHEMWAMNKIEAGWM--- 896
Db    201 YYQYRAEDDTGCEADEITHHLQATAQRYLHIVYYGNRTASETLPGLDGSAPSQADWLFYL 260

Qy    897 ---YGDQREDLHKIHPCLVPFERLPPA-------------EKRYDIQLAVQTLKT----- 935
Db    261 VFDYGERSNNL-----------KTPPAFSTTGSWLCRQDRFSRYEYGFEIRTRRLCRQVL 309

Qy    936 ----ILALGYYISLDKPPARIRNVRLPNEP--------FMQSNGYKP-------APLDLS 976
Db    310 MYHHLQALDSKITEHNGPTLVSRLILNYDESAIASTLVFVRRVGHEQDGNVVTLPPLELA 369

Qy    977 AVTLTPK-------MD-----------ELVDQLAENTHNLWARERIQQGWTYGLNEDSDM 1018
Db    370 YQDFSPRHHAHWQPMDVLANFNAIQRWQLVDLKGEGLPGLLYQDK--GAWWY-------- 419

Qy   1019 HRSPHLVPYPKVDDAIKKANR--DTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQ 1076
Db    420 ----------------RSAQRLGEIGSDAVTWEKMQPLSVIPSL--QSNASLVDINGDGQ 461

Qy   1077 ADF-------RTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSW 1129
Db    462 LDWVITGPGLRGYHSQR----PDGSW-TRFTPLNALPVEYTHPRAQLAD--LMGAGLSDL 514

Qy   1130 AFDGYNEEKVYSGNTESFGKQWAV---GDVVGVFLDLID--KTISFSLNGELLMDALG-G 1183
Db    515 VLIGPKSVRLYANTRDGFAKGKDVVQSGDIT-LPVPGADPRKLVAFS-------DVLGSG 566

Qy   1184 ETTFADVQGDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNM------ 1237
Db    567 QAHLVEVSATKVTCWPNLGRGR-----FGQPI-TLPGFSQPATE--FNPAQVYLADLDGS 618

Qy   1238 -KRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHN---TFETMEKANW 1293
Db    619 GPTDLIYVHTNRLDIFLNKSGNGFAEPVTLRFPEG------LRFDHTCQLQMADVQGLGV 672

Qy   1294 EFLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMND 1353
Db    673 ASLILSVPHMSPHHWRCDLTNMKPW---------LLNE-------------------MNN 704

Qy   1354 IKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEM 1413
Db    705 NMGVHHTLRYR---SSSQFWLDE---KAAALTTGQTPVCY---LPFPIHTLWQTETEDEI 755

Qy   1414 A--------KYDLGAQGLTPDDKKDKRGRSPFKFF---------RSKRGESSDRAKSRKS 1456
Db    756 SGNKLVTTLRYARGAW--------DGRERE-FRGFGYVEQTDSHQLAQGNAPERTPPALT 806

Qy   1457 K----TPDPFSDTEV--------------SPERGARRPNPQIKVS--QANQRY---NGMN 1493
Db    807 KNWYATGLPVIDNALSTEYWRDDQAFAGFSPRFTTWQDNKDVPLTPEDDNSRYWFNRALK 866

Qy   1494 ARPSRTNLYGSQVGLNMATP---------------TQDRKQMTTSTLAQSATETVGNEIF 1538
Db    867 GQLLRSELYGLDDSTNKHVPYTVTEFRSQVRRLQHTDSRYPVLWSSVVESRNYHYERIAS 926

Qy   1539 DAEC--------------LKLINEYF-----YGVRIYPGQDP----------------T 1562
Db    927 DPQCSQNITLSSDRFGQPLKQLSVQYPRRQPAINLYPDTLPDKLLANSYDDQQRQLRLT 986

Qy   1563 HVYIGWVTTQYHLHSK-------------------------DFNQSKVTKSSVIITDDY 1596
Db    987 YQQSSW----HHLTNNTVRVLGLPDSTRSDIFTYGAENVPAGGLNLELLSDKNSLIADDK 1042

Qy   1597 DR-----------------VVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSV 1639
Db   1043 PREYLGQQKTAYTDGQNTTPLQTPTRQALIAFTETTVFNQ-----STLSAFNGSIPSDKL 1097

Qy   1640 DTSTGSVSFTCEGKDTSFKFKMEPETKLFPA----------------------------- 1670
Db   1098 STTLEQAGY----QQTNYLFPRTGEDKVWVAHHGYTDYGTAAQFWRPQKQSNTQLTGKIT 1153

Qy   1671 --------IFVEA------------------TSKEILQIE----------LGRSAT----- 1690
Db   1154 LIWDANYCVVVQTRDAAGLTTSAKYDWRFLTPVQLTDINDNQHLITLDALGRPITLRFWG 1213

Qy   1691 ---------SLPLSAAVLPTSDKHVIPQFPPRLKV---QCLKPHQWA---------RVPN 1729
Db   1214 TENGKMTGYSSPEKASFSPPSDVNAAIELKKPLPVAQCQVYAPESWMPVLSQKTFNRLAE 1273

Qy   1730 QSLQVHALKLSDIRGWSMLCEDA-VSMLALH--IPEEDRCIDILEPIEMDKLLSFHSHTL 1786
Db   1274 QDWQ----KLYNAR---IITEDGRICTLAYRRWVQSQKAIPQLISLLNNGPRLPPHSLTL 1326

Qy   1787 TLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTM 1846
Db   1327 T-------TDRY-------DHDPEQQ----IRQQVV---FSDGFGRLLQA--AARHEAGM 1363

Qy   1847 EACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISN------ 1900
Db   1364 ARQRNE---------------DGSLIINVQHTEN---RWAVT----GRTEYDNKGQPIR 1400

Qy   1901 LYSPYFPLE---VAREFVMQALAEAVETNQVHNRDPVGGS----------NENLFLPLIK 1947
Db   1401 TYQPYFLNDWRYVSNDSARQEKEAYADT---HVYDPIGREIKVITAKGWFRRTLFTPWFT 1457

Qy   1948 LVDRLLLVGMMRDE-----DVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHM--KMAEGA 2000
Db   1458 VNE---------DENDTAAEVKKVKM--------PGSDNKGQTIRTRPMKNIDPKLYQKT 1500

Qy   2001 KLQMCY-----LLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEI----KQSDLP 2051
Db   1501 PTVSVYDNRGLIIRNID----FHRTTA---------NGDPDTRITRHQYDIHGHLNQSIDP 1548

Qy   2052 SAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCP-CGEELIA----RMNEFHDTLMA 2106
Db   1549 RLYEAKQT-----------NNTIKPNFLWQYDLTGNPLCTESIDAGRTVTLNDIEGRPLL 1597

Qy   2107 HVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKV 2166
Db   1598 TVTATGVIQ---TRQYETSSLP---GRLLSV------------------AEQTPEEKTSRI 1634

Qy   2167 LIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVG-ELIRALEKTYVI---NAKTKLDVA 2222
Db   1635 TERLI--WAGNTEAEKD---HNLAGQCVRHYDTAGVTRLESLSLTGTVLSQSSQLLIDTQ 1689

Qy   2223 EM-WVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQH---PDLIRVLRVHENVMA 2278
Db   1690 EANWTG-----------------------------DNETVWQNMLADDIYTTLSTFDATGA 1721
```





RESULT 11
US-11-056-355B-86482
; Sequence 86482, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86482
; LENGTH: 1703
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(1703)
; OTHER INFORMATION: Ceres Seq. ID no. 12690877
US-11-056-355B-86482

Query Match 0.8%; Score 219; DB 7; Length 1703;
Best Local Similarity 18.9%; Pred. No. 0.00031;
Matches 273; Conservative 246; Mismatches 481; Indels 446; Gaps 69;



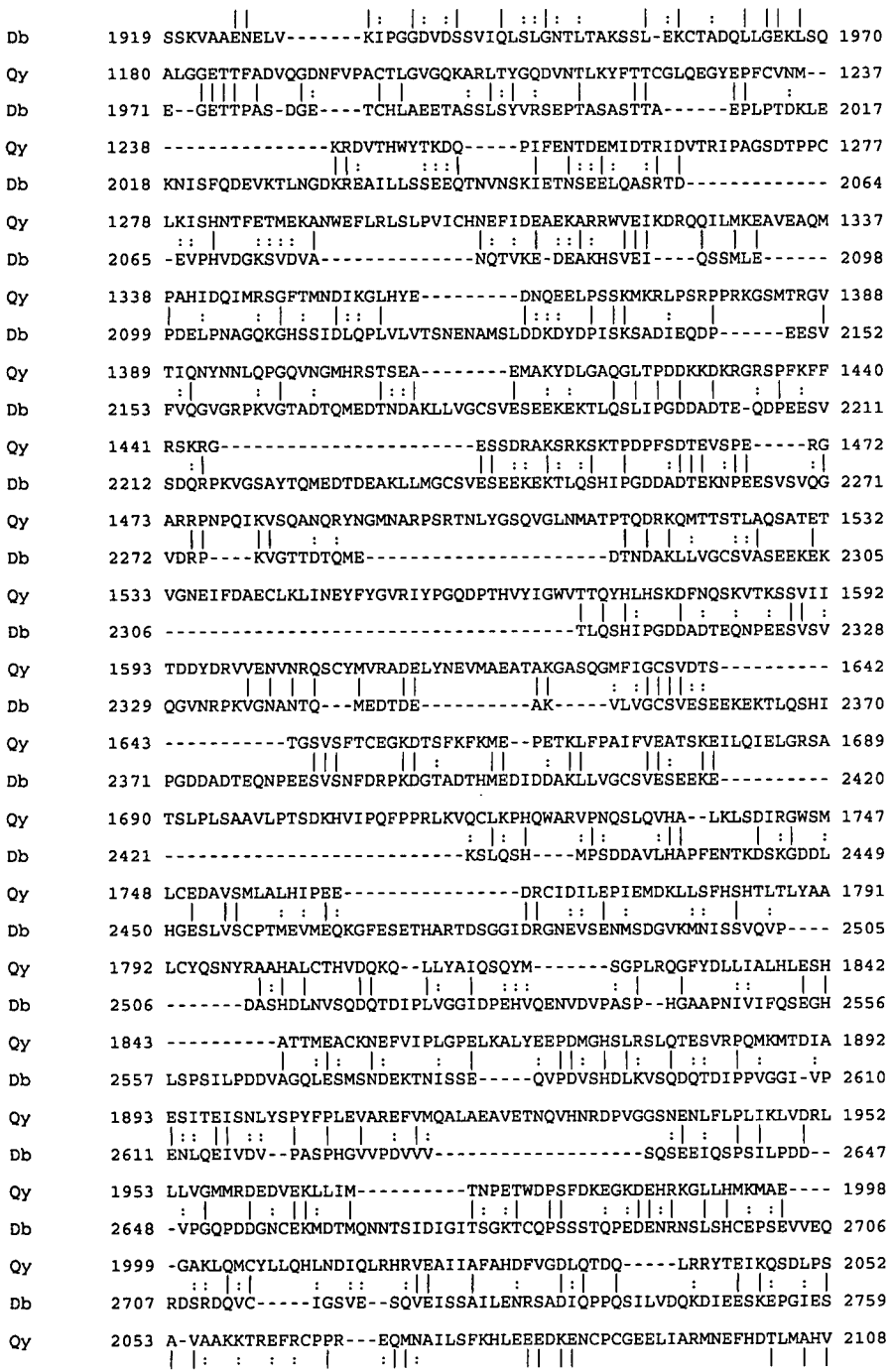
```
Db       1228 EQVKKN 1233
```

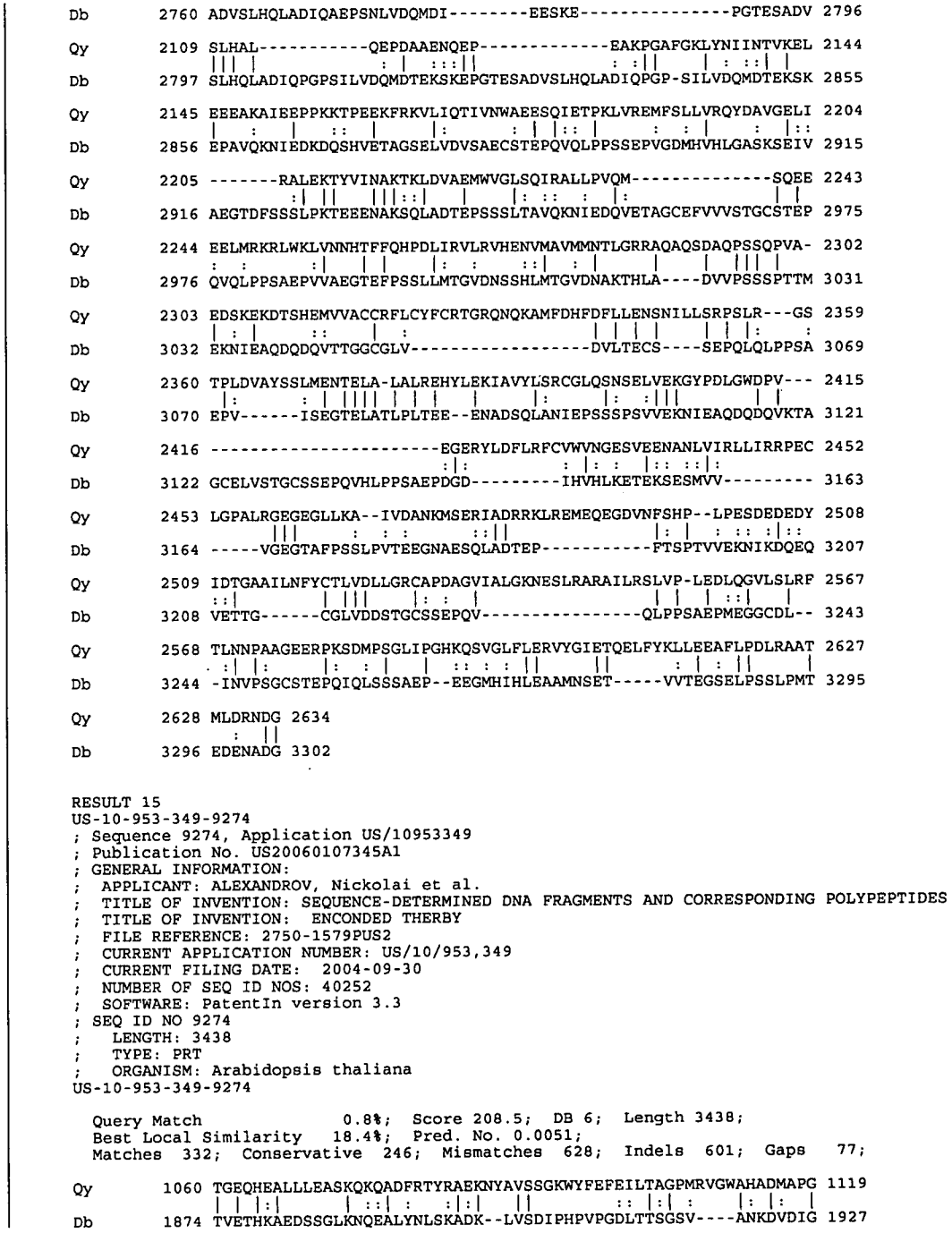
RESULT 12
US-11-056-355B-86481
; Sequence 86481, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86481
;   LENGTH: 1710
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(1710)
;   OTHER INFORMATION: Ceres Seq. ID no. 12690876
US-11-056-355B-86481

```
  Query Match             0.8%;  Score 219;  DB 7;  Length 1710;
  Best Local Similarity   18.9%;  Pred. No. 0.00031;
  Matches 273;  Conservative  246;  Mismatches  481;  Indels  446;  Gaps   69;

Qy       3083 NMKLLKPSTTFSRRSSFKTSTR---------DIKFFSKAVLPLMEKYFSTHRNYFIAVAT 3133
Db        128 NIAFMEDPQSVSSGKGFKTAKARKGLNFNNVDGKEINAKVLSESER-ASKAEAEIVALKD 186

Qy       3134 ATNNVGAASLKEKEMVAALF---CKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKSL 3190
Db        187 ALSKVQA----EKEASLAQFDQNLEKLSNLESEVSRAQEDSRVLIE------RATRAEAE 236

Qy       3191 VKNCPEFI-------RTSMLTF---FNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLG 3240
Db        237 VETLRESLSKVEVEKESSLLQYQQCLQNIAD--------------------LEDRISLA 275

Qy       3241 YINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKT 3300
Db        276 QKE-------AGEVDERANRAEAETLALKQSLVSS--------ETDKEAALVQYQQCLKT 320

Qy       3301 EIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCMP 3360
Db        321 --------------------ISNLEERLHKAEEDSRLTN------------QRAENAEG 347

Qy       3361 TLETILGEVDQFVESDKTYN-EAPHIIDVVLPLLCSYLPFWWAQG---------PDNVTP 3410
Db        348 EVESLKQKVSKLIEENEAYELQYQQCLDTIADL---KLKLFHAQEETQRLSREIEDGVAK 404

Qy       3411 TGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSF 3470
Db        405 LKFAEEKCVVLERSNQNLHSELDGLLEKLGNQ------------------SHELTEK-- 443

Qy       3471 LPLAERVRKRTDNMFH--KEESLRGFIKSST--DDTSQVESQIQEDWQLLVRDIYSFYPL 3526
Db        444 -------QKELGRLWTCVQEENLR-FMEAETAFQTLQQLHSQSQEELSTLALELQNRSQI 495

Qy       3527 LIKYVDLQ-RNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISAN------EI 3579
Db        496 L---KDMEARNNGLQEEVQEAKDQSKSLNELNLSSAASIKSLQEEVSKLRETIQKLEAEV 552

Qy       3580 DNMVLIMPTATRRVTAVTDGTPQGGGKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGL 3639
Db        553 ELRVDQRNALQQEIYCLKEELSQIG----KKHQ----------------SMVEQVELVGL 592

Qy       3640 N--LFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLG 3697
Db        593 HPESFGSSVKELQE--ENSKLKEIRERESIE--KTALI--EKLEMMEKLVQKNLLLE--N 644

Qy       3698 SKSKSNITVETAENKAKIIDDTVERIVAMSKVLFGLH-----MIDHPQQMSKN------- 3745
Db        645 SISDLNAELETIRGKLKTLE---EASMSLAEEKSGLHSEKDMLISRLQSATENSKKLSEE 701

Qy       3746 -------VYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEV 3798
Db        702 NMVLENSLFNANVELEELK--------SKLKSL--EESCHLLNDDKTTLTSERESLLSHI 751

Qy       3799 -----MIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQE-DPLY 3852
Db        752 DTMRKRIEDLEK--EHAELKVK-VLE-----------------LATERESSLQKIEELG 790

Qy       3853 MSYAHIIAKSCGEEEEEGGGEEEEGGGEA---EAEDEGRASIHEQEMEKQKLLFHQARLA 3909
Db        791 VS---LNAKDCEYASFVQFSESRMNGMESTIHHLQDENQCRVREYQVELDRA--HDAHI- 844

Qy       3910 DRGVAEMVLLHISASKGLPSEMVMKTLQLGI---SILRGGNIDIQMG--MLNHL---KDK 3961
Db        845 -----EIIVL-------------QKCLQDWLEKSSSLIAENQDIKEASKLLEKLVSELEE 886

Qy       3962 KDVGFFTSIAGLMNSCSVLDLDAFERNTKAE---GLGVGLEGAAGEKNMHDAEFTCALFR 4018
Db        887 ENIGKQVQIDSSINCIKILRTGIYQVLMKLEIIPGIGSGDENSRDQRNMHD------ILN 940

Qy       4019 FIQLTCEGHNLDWQNYL---RTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELI 4075
Db        941 RLE--------DMQTMLLSIRDENQHSAIENLVL--IEFLRQLKS--------------- 975

Qy       4076 DPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKL 4135
Db        976 ---------EAVGIETEK-KILEEELESQC----QQLSFSR--DETQKLIFVNGELTTKV 1019

Qy       4136 SKHSSQVDLL--------KELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNV 4187
Db       1020 NQGVNREKVLMVEIEDFHRQVLQLRDDY----------------------TILQGDNNK 1056

Qy       4188 ELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACC 4247
Db       1057 TLDEKAY--------LTKSTL------------------QLEEEKCKLEDDISLLLS-- 1087

Qy       4248 ETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFE 4307
Db       1088 ETIYQS--------------------NLIILLEDV------------ILEKLSGAMKLNE 1115

Qy       4308 PFLGRIEIMGG--SKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSI------------ 4353
Db       1116 D-LDRLSIVKCKLEEEVRELGDKLKSADIANFQLQVVLEKSNAELLSARSANVHLEHEIA 1174

Qy       4354 -VTEGGDKEKLEA--FVNFCEDAIFEMTHA-SGLMAASEESVGGTKNREASYMYMGDDDD 4409
Db       1175 NVKVQKEKELLEAMLMISIMQNEKSELSKAVEGLECRYKEAKAIEEDRDKQVLRLRGDYD 1234

Qy       4410 ERAGKD 4415
Db       1235 EQVKKN 1240
```

RESULT 13
US-11-056-355B-86480
; Sequence 86480, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14

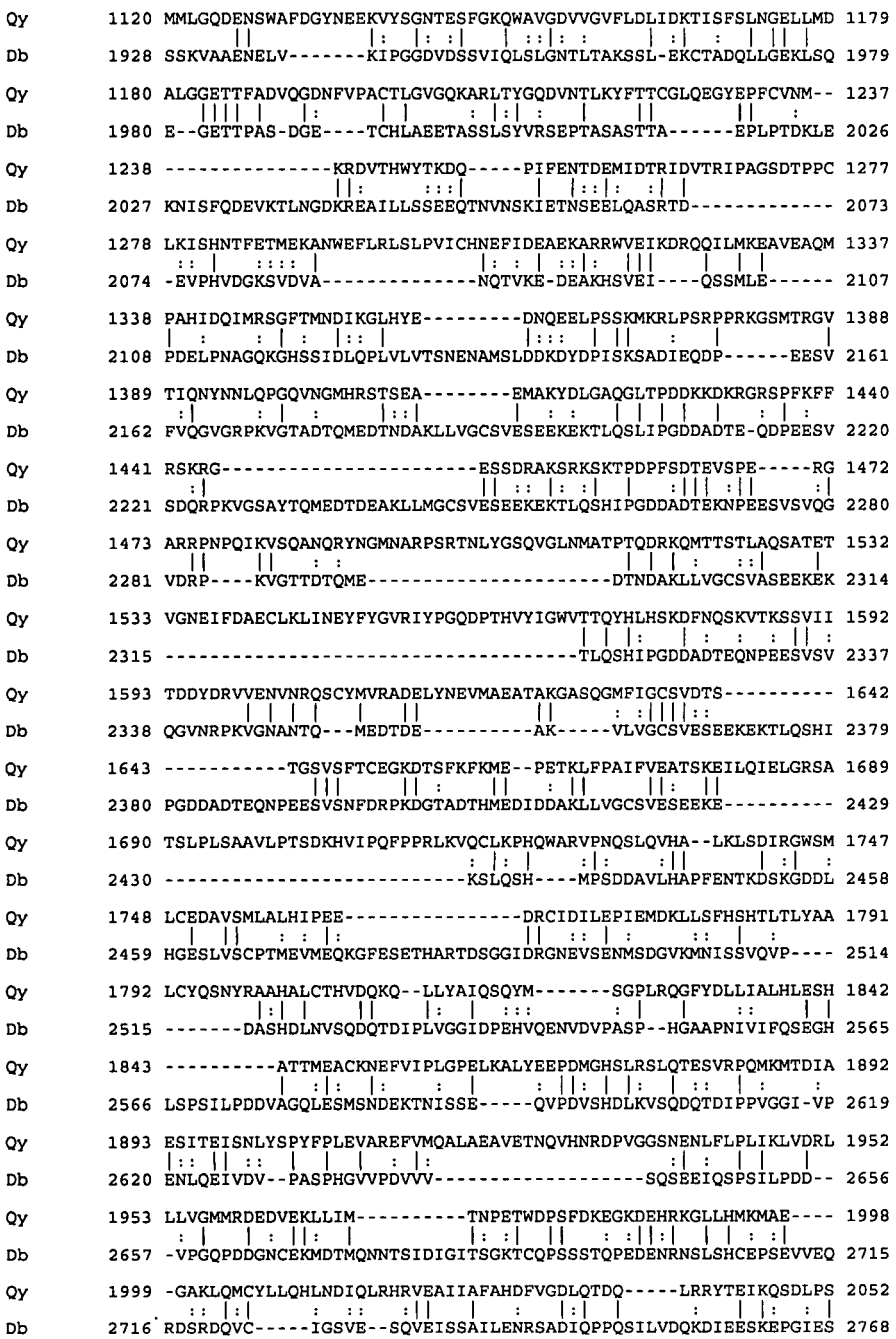
```
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86480
;   LENGTH: 1744
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(1744)
;   OTHER INFORMATION: Ceres Seq. ID no. 12690875
US-11-056-355B-86480

  Query Match             0.8%;  Score 219;  DB 7;  Length 1744;
  Best Local Similarity   18.9%;  Pred. No. 0.00032;
  Matches  273;  Conservative  246;  Mismatches  481;  Indels  446;  Gaps   69;

Qy       3083 NMKLLKPSTTFSRRSSFKTSTR---------DIKFFSKAVLPLMEKYFSTHRNYFIAVAT 3133
                :  ::   : |   |||:           | |  :  ||   |:  |       :|:
Db        162 NIAFMEDPQSVSSGKGFKTAKARKGLNFNNVDGKEINAKVLSESER-ASKAEAEIVALKD 220

Qy       3134 ATNNVGAASLKEKEMVAALF---CKLASLLRSRLAAFGPDVRITVRCLQVLVKGIDAKSL 3190
                | : | |    |||   | |    :  | | | ::   | |: :      :   |::
Db        221 ALSKVQA----EKEASLAQFDQNLEKLSNLESEVSRAQEDSRVLIE------RATRAEAE 270

Qy       3191 VKNCPEFI-------RTSMLTF---FNNVADDVGHTIMNLQDGKYAHLRGTHLKTSTSLG 3240
                |:   | :        :|:| :     |:||                  |:   ||
Db        271 VETLRESLSKVEVEKESSLLQYQQCLQNIAD--------------------LEDRISLA 309

Qy       3241 YINGVLLPILTAKFDHLANCEYGADLLLDEIQVASYKMLGSLYALGTDASLTHDRKYLKT 3300
                       : |  ||       | | :  |:|            :|:|   :: |||
Db        310 QKE-------AGEVDERANRAEAETLALKQSLVSS--------ETDKEAALVQYQQCLKT 354

Qy       3301 EIERHKPALGSCLGAFSSTFPVAFLEPHLNKHNQFSLLNRIADHSLEAQDIMQKMEQCMP 3360
                              :: ||  |:|  : | |            |: |
Db        355 --------------------ISNLEERLHKAEEDSRLTN-----------QRAENAEG 381

Qy       3361 TLETILGEVDQFVESDKTYN-EAPHIIDVVLPLLCSYLPFWWAQG---------PDNVTP 3410
                :|::  :| : :| :: |  :    :| :  |    |  : ||          | |
Db        382 EVESLKQKVSKLIEENEAYELQYQQCLDTIADL---KLKLFHAQEETQRLSREIEDGVAK 438

Qy       3411 TGGNHVTMVTAEHMNQLLKNVLKLIKKNIGNENAPWMTRIATYTQQIIINSSEELLRDSF 3470
                    |  | || | : |  : : :||:                  | ||
Db        439 LKFAEEKCVVLERSNQNLHSELDGLLEKLGNQ-----------------SHELTEK-- 477

Qy       3471 LPLAERVRKRTDNMFH--KEESLRGFIKSST--DDTSQVESQIQEDWQLLVRDIYSFYPL 3526
                    :|    ::   :||:|| |::: |      |: || ||:   |  :: :   :
Db        478 -------QKELGRLWTCVQEENLR-FMEAETAFQTLQQLHSQSQEELSTLALELQNRSQI 529

Qy       3527 LIKYVDLQ-RNHWLRNNVPEAEELYNHVAEIFNIWSKSQYFLKEEQNFISAN------EI 3579
                |    |:: ||: |:  | ||::    : |:    : |   |:|| : :          |:
Db        530 L---KDMEARNNGLQEEVQEAKDQSKSLNELNLSSAASIKSLQEEVSKLRETIQKLEAEV 586

Qy       3580 DNMVLIMPTATRRVTAVTDGTPQGGGKKKKKHRDKKRDKDKEVQASLMVACLKRLLPVGL 3639
                :  |       : :  : :   | |    |||:                 : ::::  |||
Db        587 ELRVDQRNALQQEIYCLKEELSQIG----KKHQ----------------SMVEQVELVGL 626

Qy       3640 N--LFAGREQELVQHCKDRFLKKMSEQDVAEFAKTQLTLPDKIDPADEMSWQHYLYSKLG 3697
                :   |    :|| :  ::  ||:: |::  |  || |   :|::  :::  :: |
Db        627 HPESFGSSVKELQE--ENSKLKEIRERESIE--KTALI--EKLEMMEKLVQKNLLLE--N 678

Qy       3698 SKSKSNITVETAENKAKIIDDTVERIVAMSKVLFGLH-----MIDHPQQMSKN------- 3745
                | |  |  :||    | | ::   |  :::::   |||     :|   |  ::|
Db        679 SISDLNAELETIRGKLKTLE---EASMSLAEEKSGLHSEKDMLISRLQSATENSKKLSEE 735

Qy       3746 -------VYRSVVSIQRKRAVIACFRQTSLHSLPRHRACNIFARTYYELWLEEENIGQEV 3798
                      :: : | ::  :       : | ||    :|::       |  | |::   :
Db        736 NMVLENSLFNANVELEELK--------SKLKSL--EESCHLLNDDKTTLTSERESLLSHI 785

Qy       3799 -----MIEDLTQSFEDAELKKSDVVEEGEKPDPLTQLVTTFCRGAMTERSGALQE-DPLY 3852
                    |||| :  | ||||   |:|                   |||  :||: : |
Db        786 DTMRKRIEDLEK--EHAELKVK-VLE-----------------LATERESSLQKIEELG 824

Qy       3853 MSYAHIIAKSCGEEEEEGGGEEEEGGGEA---EAEDEGRASIHEQEMEKQKLLFHQARLA 3909
                :|   : || |           |     | |:     :|| :  : | ::|  :   | | :
Db        825 VS---LNAKDCEYASFVQFSESRMNGMESTIHHLQDENQCRVREYQVELDRA--HDAHI- 878

Qy       3910 DRGVAEMVLLHISASKGLPSEMVMKTLQLGI---SILRGGNIDIQMG--MLNHL---KDK 3961
                    |:::|             | ||  :   | |   | ||:    :| |    ::
Db        879 -----EIIVL-------------QKCLQDWLEKSSSLIAENQDIKEASKLLEKLVSELEE 920

Qy       3962 KDVGFFTSIAGLMNSCSVLDLDAFERNTKAE---GLGVGLEGAAGEKNMHDAEFTCALFR 4018
                :::|    |   :|   :|    ::   | |   |:| | | :  ::||||      :
Db        921 ENIGKQVQIDSSINCIKILRTGIYQVLMKLEIIPGIGSGDENSRDQRNMHD------ILN 974

Qy       4019 FIQLTCEGHNLDWQNYL---RTQAGNTTTVNVVICTVDYLLRLQESIMDFYWHYSSKELI 4075
                 ::         | |  |   | :  ::   |:|:  :::| :|:
Db        975 RLE--------DMQTMLLSIRDENQHSAIENLVL--IEFLRQLKS-------------- 1009

Qy       4076 DPAGKANFFKAIGVASQVFNTLTEVIQGPCTQNQQALAHSRLWDAVGGFLFLFSHMQDKL 4135
                       :|:|: ::    | | ::  |    | |: ||  |     :|:    : |:
Db       1010 ---------EAVGIETEK-KILEEELESQC----QQLSFSR--DETQKLIFVNGELTTKV 1053

Qy       4136 SKHSSQVDLL--------KELLNLQKDMIPMMLSMLEGNVVNGTIGKQMVDTLVESASNV 4187
                 ::  ::  :|        :::| |: |                          |:::  :|
Db       1054 NQGVNREKVLMVEIEDFHRQVLQLRDDY----------------------TILQGDNNK 1090

Qy       4188 ELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEKMEQQKSYTPEEIEFLLACC 4247
                 | | :        || |                        ::|::|    ::|  ||:
Db       1091 TLDEKAY--------LTKSTL------------------QLEEEKCKLEDDISLLLS-- 1121

Qy       4248 ETNHDGKLDYIGFCDRFHEPAKEIGFNLAVLLTNLSEHMPNEPRLARFLETAGSVLNYFE 4307
                 || :                  || |:|| ::              ||     : |
Db       1122 ETIYQS-------------------NLIILLEDV------------ILEKLSGAMKLNE 1149

Qy       4308 PFLGRIEIMGG--SKRIERVYFEIKESNIEQWEKPQIKESKRAFFYSI------------ 4353
                  | |: |:     : :  :  ::| ::|  ::   : |    |   |
Db       1150 D-LDRLSIVKCKLEEEVRELGDKLKSADIANFQLQVVLEKSNAELLSARSANVHLEHEIA 1208

Qy       4354 -VTEGGDKEKLEA--FVNFCEDAIFEMTHA-SGLMAASEESVGGTKNREASYMYMGDDDD 4409
                  |    :|| |||   ::  ::   |:: |  ||    :|:    ::|:   : | |
Db       1209 NVKVQKEKELLEAMLMISIMQNEKSELSKAVEGLECRYKEAKAIEEDRDKQVLRLRGDYD 1268

Qy       4410 ERAGKD 4415
                 |:  |:
Db       1269 EQVKKN 1274


RESULT 14
US-10-953-349-9275
; Sequence 9275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9275
;   LENGTH: 3429
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9275

  Query Match             0.8%;  Score 208.5;  DB 6;  Length 3429;
  Best Local Similarity   18.4%;  Pred. No. 0.0051;
  Matches  332;  Conservative  246;  Mismatches  628;  Indels  601;  Gaps   77;

Qy       1060 TGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPG 1119
                | | |:|       | ::| :   :|:|    ||         :: |:| :    |: |:  |
Db       1865 TVETHKAEDSSGLKNQEALYNLSKADK--LVSDIPHPVPGDLTTSGSV----ANKDVDIG 1918

Qy       1120 MMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMD 1179
```

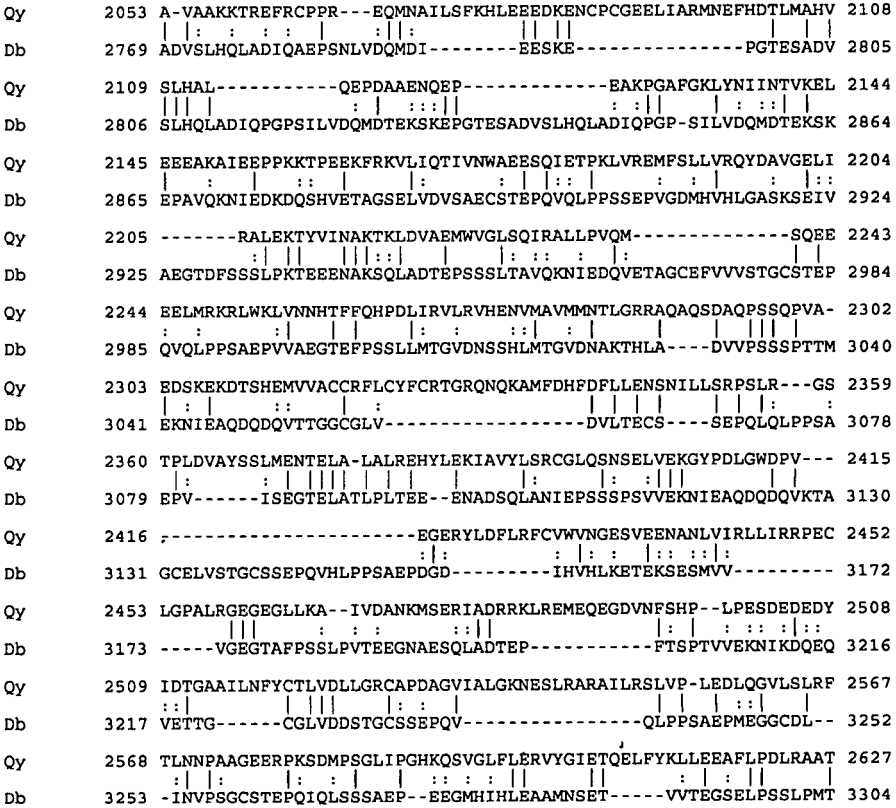




RESULT 15
US-10-953-349-9274
; Sequence 9274, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9274
; LENGTH: 3438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9274

Query Match 0.8%; Score 208.5; DB 6; Length 3438;
Best Local Similarity 18.4%; Pred. No. 0.0051;
Matches 332; Conservative 246; Mismatches 628; Indels 601; Gaps 77;





Search completed: October 7, 2006, 00:10:38
Job time : 164 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: October 10, 2006, 15:44:08 ; Search time 854 Seconds
(without alignments)
10954.970 Million cell updates/sec

Title: US-10-668-767-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 ctaaattcgaaattcccatc.....ggtgaccacccagtaccact 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

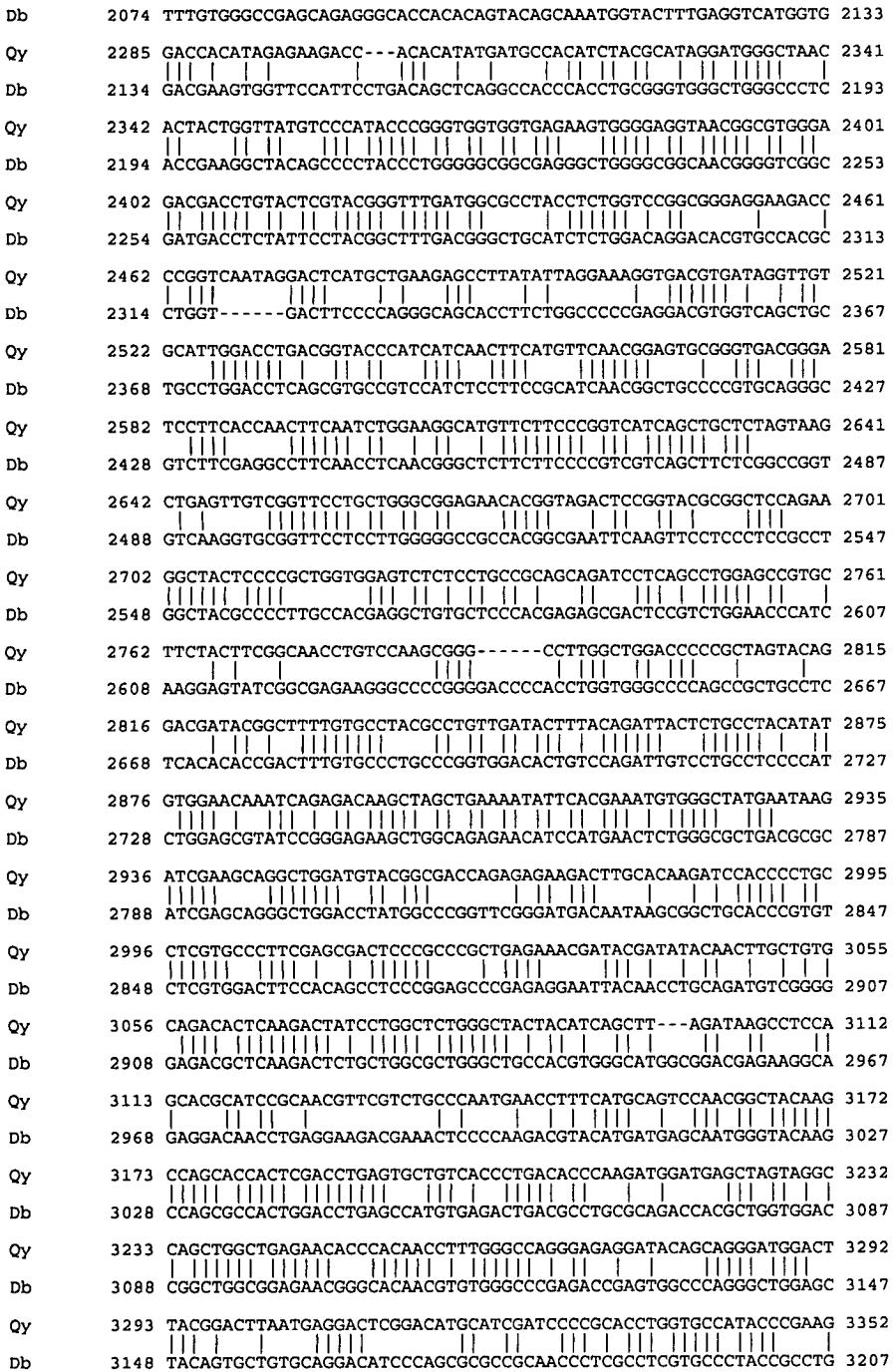
SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	869.4	17.4	15378	3	US-08-785-420-1	Sequence 1, Appli
	2	840.8	16.8	4078	3	US-09-016-434-1154	Sequence 1154, Ap
	3	809	16.2	15572	3	US-09-424-783-1	Sequence 1, Appli
	4	65.6	1.3	1050	2	US-08-480-481-4	Sequence 4, Appli
	5	64	1.3	1050	2	US-08-480-481-3	Sequence 3, Appli
	6	53.6	1.1	1598	3	US-08-785-420-3	Sequence 3, Appli
c	7	51.6	1.0	7218	2	US-08-232-463-14	Sequence 14, Appl
	8	51	1.0	900	2	US-08-480-481-6	Sequence 6, Appli
	9	40.8	0.8	1334	3	US-09-668-097A-35	Sequence 35, Appl
	10	39.4	0.8	294	3	US-09-252-991A-11838	Sequence 11838, A
	11	38.6	0.8	1768	3	US-09-485-529-13	Sequence 13, Appl
	12	38.6	0.8	2125	3	US-09-485-529-14	Sequence 14, Appl
	13	38.2	0.8	1290	3	US-09-902-540-5006	Sequence 5006, Ap
	14	38.2	0.8	12950	3	US-09-902-540-1036	Sequence 1036, Ap
	15	37.8	0.8	399	3	US-09-621-976-8976	Sequence 8976, Ap
	16	37.6	0.8	1738	3	US-10-164-595-31	Sequence 31, Appl
c	17	37.2	0.7	34534	3	US-09-949-016-15141	Sequence 15141, A
c	18	37	0.7	474	3	US-09-621-976-18033	Sequence 18033, A
	19	36.8	0.7	711	5	US-09-974-300-310	Sequence 310, App
	20	36.8	0.7	1599	3	US-09-902-540-8406	Sequence 8406, Ap
c	21	36.8	0.7	7581	3	US-09-902-540-882	Sequence 882, App
	22	36.6	0.7	1750	3	US-10-104-047-1424	Sequence 1424, Ap
c	23	36.4	0.7	650	3	US-09-533-559-306	Sequence 306, App
	24	36.4	0.7	3778	3	US-09-799-451-160	Sequence 160, App
	25	36.4	0.7	4376	3	US-10-200-012-15	Sequence 15, Appl
	26	36.4	0.7	46288	3	US-09-949-016-14999	Sequence 14999, A
	27	36.4	0.7	46311	3	US-09-949-016-15000	Sequence 15000, A
	28	36.2	0.7	807	3	US-09-252-991A-6077	Sequence 6077, Ap
	29	36.2	0.7	2406	3	US-09-252-991A-6158	Sequence 6158, Ap
	30	36	0.7	49377	2	US-08-764-233A-1	Sequence 1, Appli
	31	35.8	0.7	630	3	US-09-252-991A-11354	Sequence 11354, A
c	32	35.8	0.7	912	3	US-09-252-991A-11295	Sequence 11295, A
	33	35.8	0.7	948	3	US-09-252-991A-11374	Sequence 11374, A
	34	35.6	0.7	900	3	US-09-902-540-6576	Sequence 6576, Ap
	35	35.6	0.7	2055	4	US-10-094-749-464	Sequence 464, App
c	36	35.6	0.7	3889	3	US-09-902-540-492	Sequence 492, App
c	37	35.6	0.7	194933	3	US-09-949-016-14172	Sequence 14172, A
	38	35.4	0.7	1122	3	US-09-252-991A-7810	Sequence 7810, Ap
c	39	35.4	0.7	1141	3	US-09-806-708B-22	Sequence 22, Appl
	40	35.4	0.7	1389	3	US-09-252-991A-7948	Sequence 7948, Ap
	41	35.4	0.7	1839	2	US-08-272-875-1	Sequence 1, Appli
	42	35.4	0.7	1839	2	US-08-272-875-2	Sequence 2, Appli
c	43	35.4	0.7	1947	3	US-09-252-991A-7533	Sequence 7533, Ap
c	44	35.4	0.7	2422	3	US-09-369-247-53	Sequence 53, Appl
c	45	35.4	0.7	2422	3	US-10-062-548-53	Sequence 53, Appl

ALIGNMENTS

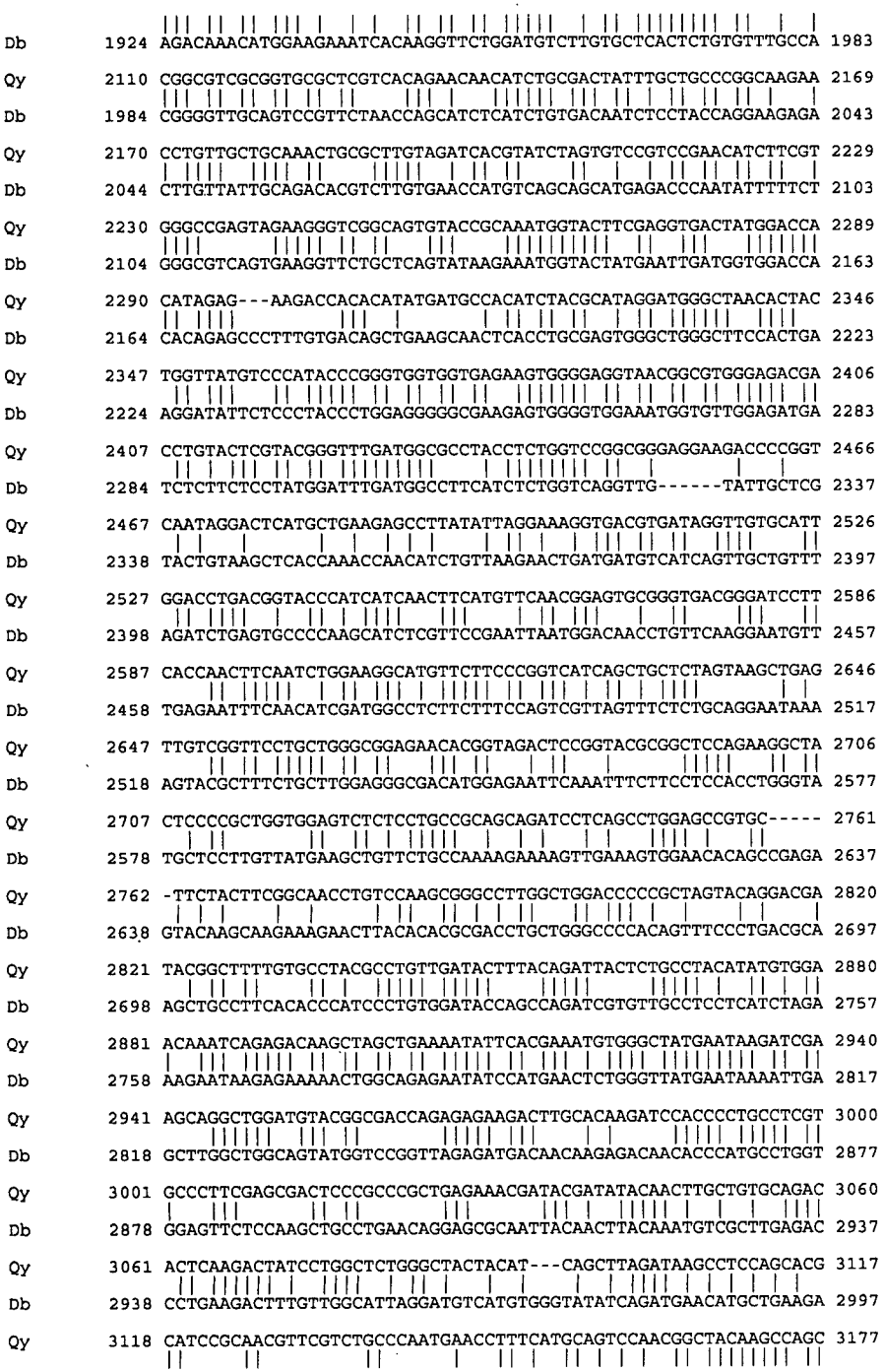
```
RESULT 1
US-08-785-420-1
; Sequence 1, Application US/08785420
; Patent No. 6001976
;  GENERAL INFORMATION:
;    APPLICANT:  MacLennan, David H
;    APPLICANT:  O'Brien, Peter J.
;    TITLE OF INVENTION:  DIAGNOSIS FOR PORCINE MALIGNANT
;    TITLE OF INVENTION:  HYPERTHERMIA
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte,
;      STATE:  No. 6001976th Carolina 28234
;      COUNTRY:  U.S.A.
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,420
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,388
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/030,159
;      FILING DATE:  15-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Layton,Jr., Samuel G.
;      REGISTRATION NUMBER:  22807
;      REFERENCE/DOCKET NUMBER:  3477-73
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-377-1561
;      TELEFAX:  704-334-2014
;      TELEX:  57-5102
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15378 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
```

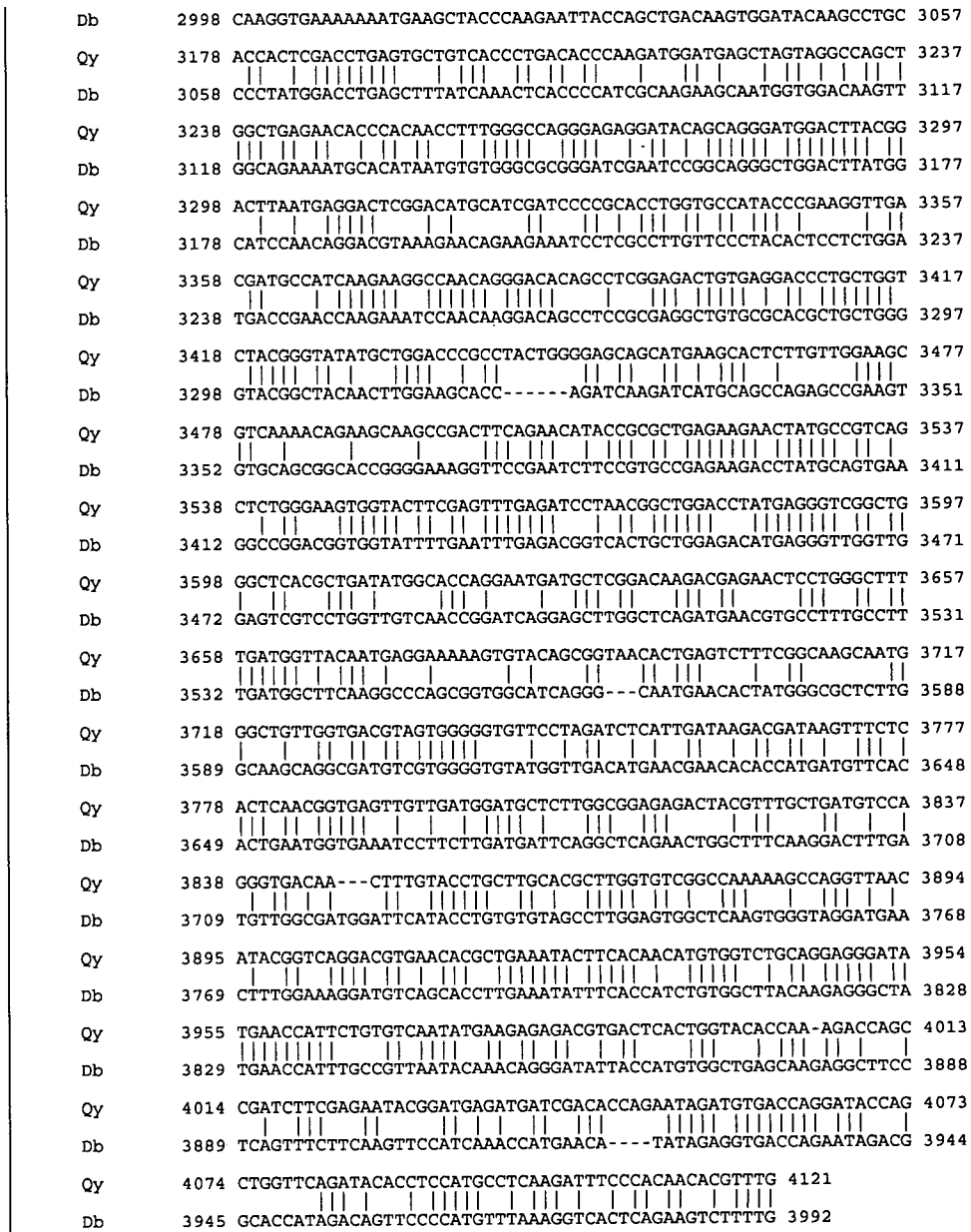
```
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Porcine RYR1 Gene
;    POSITION IN GENOME:
;      UNITS:  bp
US-08-785-420-1

  Query Match             17.4%;  Score 869.4;  DB 3;  Length 15378;
  Best Local Similarity   55.3%;  Pred. No. 4.6e-261;
  Matches 2099;  Conservative    0;  Mismatches 1591;  Indels  105;  Gaps   17;

Qy        269 GGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAAGACATGGTGTGCATGTCG 328
Db        139 GGAGGAGAGGGCGAAGATGAGGTCCAGTTTCTGCGGACAGACGACGAGGTGGTCCTGCAG 198

Qy        329 TGCACAGCGACAGGAGAGAGGG------------TGTGCCTGGCTGCCGAAGGTCTCGGC 376
Db        199 TGCAACGCTACGGTGCTCAAGGAGCAGCTCAAGCTCTGCCTGGCCGCCGAGGGCTTCGGC 258

Qy        377 AACCGGCACTGCTTCCTGGAG---AATATTGCCGACAAGAACATACCGCCTGATCTGTCG 433
Db        259 AACCGCCTCTGCTTCCTGGAACCCACCAGCAACGCCCAGAATGTGCCCCCCGATCTGGCC 318

Qy        434 CAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACA 493
Db        319 ATCTGCTGCTTCGTCCTGGAGCAGTCCCTGTCCGTCCGAGCCCTGCAGGAGATGCT---- 374

Qy        494 GCTGCGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGT 553
Db        375 --------GGCCAACACCGTGGAGGCCGGCGTGGAGTCATCCCAGGGCGGGGGCCATAGG 426

Qy        554 ACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCC 613
Db        427 ACGCTCTTGTATGGCCACGCCATCCTGCTCCGGCACGCGCACAGTGGCATGTATCTGAGC 486

Qy        614 TGCCTGTCAACATCATCATCCCAG---GATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 670
Db        487 TGCCTCACCACCTCCCGTTCCATGACTGACAAGCTGGCCTTCGACGTGGGACTGCAGGAG 546

Qy        671 CACTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 730
Db        547 GATGCGACAGGAGAGGCCTGTTGGTGGACTACACACCCGGCCTCCAAGCAGAGGTCGGAA 606

Qy        731 GGCGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATAC 790
Db        607 GGAGAGAAGGTTCGAGTAGGGGATGACCTCATCCTCGTCAGTGTCTCCTCTGAGCGTTAC 666

Qy        791 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCAC 850
Db        667 CTGCACCTGTCGACAGCCAGTGGGGAGCTCCAGGTTGACGCCTCCTTCATGCAGACACTG 726

Qy        851 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTC 910
Db        727 TGGAACATGAACCCCATCTGCTCTGGCTGTG------------AAGAAGGCTATGTGACT 774

Qy        911 GGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACT 970
Db        775 GGGGGTCACGTCCTCCGCCTCTTTCACGGACACATGGATGAGTGCCTGACCATCTCCCCC 834

Qy        971 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAA 1030
Db        835 GCTGACAGTGATGACCAGCGCAGACTTGTCTACTACGAGGGTGGATCTGTGTGCACCCAC 894

Qy       1031 GCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 1090
Db        895 GCCCGCTCCCTCTGGAGACTGGAACCGCTGAGAATCAGCTGGAGTGGGAGCCACCTGCGC 954

Qy       1091 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGAC 1150
Db        955 TGGGGCCAGCCGCTTCGCATCCGGCATGTCACCACCGGGAGGTACCTGGCGCTCATCGAG 1014

Qy       1151 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGC 1210

Db       1015 GACCAGGGCCTGGTGGTGGTTGATGCCAGCAAGGCCCACACCAAGGCCACCTCCTTCTGT 1074

Qy       1211 CTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1270
Db       1075 TTCCGCATTTCCAAGGAGAAGCTGGATACGGCCCCCAAG---CGGGACGTGGAGGGCATG 1131

Qy       1271 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGC 1330
Db       1132 GGCCCCCCTGAGATCAAGTATGGGGAGTCACTGTGCTTCGTGCAGCATGTGGCCTCGGGC 1191

Qy       1331 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAG 1390
Db       1192 CTGTGGCTTACCTATGCTGCCCCAGACCCCAAGGCCCTGCGGCTCGG---CGTGCTCAAG 1248

Qy       1391 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCA 1450
Db       1249 AAGAAGGCCATTCTGCACCAGGAAGGCCACATGGACGATGCACTGTCACTGACCCGCTGT 1308

Qy       1451 CAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAG 1510
Db       1309 CAGCAGGAGGAGTCCCAGGCGGCCCGCATGATCTATAGCACTGCTGGCCTCTACAACCAC 1368

Qy       1511 TTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTC------TTC 1564
Db       1369 TTCATCAAGGGCCTGGACAGCTTCAGCGGAAAGCCACGGGGCTCTGGGGCCCCGGCTGGC 1428

Qy       1565 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCA 1624
Db       1429 ACAGCGCTACCCCTCGAGGGCGTCATCCTGAGCCTGCAGGACCTCATCGGCTACTTTGAG 1488

Qy       1625 CAGCCCGATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1684
Db       1489 CCGCCCTCGGAAGAGCTGCAGCACGAGGAGAAGCAGAGCAAGCTGCGCAGCCTGCGCAAC 1548

Qy       1685 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1744
Db       1549 CGCCAGAGCCTCTTCCAGGAGGAGGGGATGCTCTCCCTGGTCCTGAATTGCATTGACCGC 1608

Qy       1745 ATCAACGTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGA 1804
Db       1609 CTAAATGTCTACACCACTGCTGCCCACTTTGCTGAGTTT---GCAGGAGAGGAGGCAGCC 1665

Qy       1805 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGC 1864
Db       1666 GAGTCCTGGAAAGAGATTGTGAACCTGCTGTATGAGATCCTGGCCTCTCTGATCCGTGGC 1725

Qy       1865 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGC 1924
Db       1726 AATCGTGCCAACTGTGCCCTTTTCTCCAA------------CAACTTGGATTGGCTGGTC 1773

Qy       1925 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTC 1984
Db       1774 AGCAAGCTGGATCGACTGGAGGCCTCCTCAGGGATCCTGGAGGTGCTGTACTGTGTCCTG 1833

Qy       1985 ATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 2044
Db       1834 ATTGAGAGTCCTGAGGTCCTGAACATCATCCAGGAGAACCACATCAAGTCCATCATCTCC 1893

Qy       2045 CTATTAGAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTC 2104
Db       1894 CTTCTGGACAAGCATGGGAGGAACCACAAGGTGCTGGATGTCCTGTGTTCCCTGTGTGTG 1953

Qy       2105 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGC 2164
Db       1954 TGCAATGGTGTGGCCGTGTGCTCCAACCAAGATCTCATTACTGAGAACTTGCTCCCTGGC 2013

Qy       2165 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 2224
Db       2014 CGCGAGCTTCTGCTGCAGACAAACCTCATCAACTATGTCACCAGCATCCGCCCCAACATC 2073

Qy       2225 TTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 2284
```



RESULT 2
US-09-016-434-1154
; Sequence 1154, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

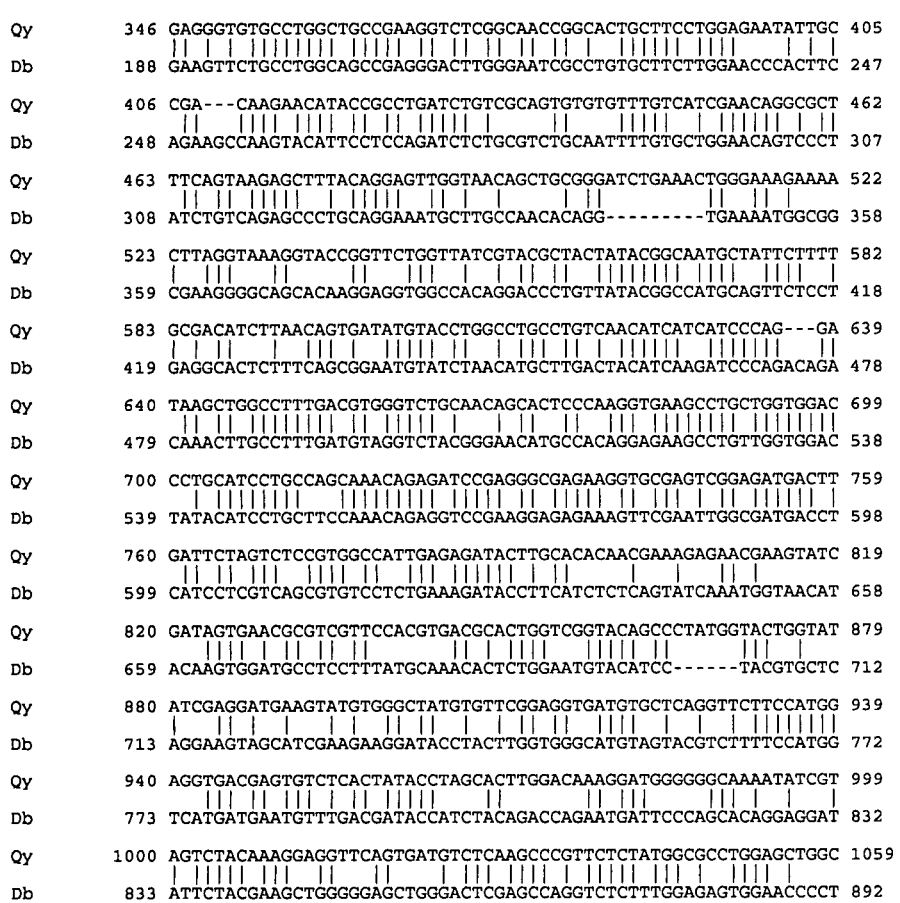
```
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1154:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4078 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1526977
US-09-016-434-1154

  Query Match             16.8%;  Score 840.8;  DB 3;  Length 4078;
  Best Local Similarity   55.0%;  Pred. No. 1.7e-252;
  Matches 2105;  Conservative    0;  Mismatches 1622;  Indels  101;  Gaps   19;

Qy        343 AGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCACTGCTTCCTGGAGAATAT 402
Db        217 ACAGAAGCTATGCTTGGCAGCAGAAGGATTTGGCAACAGACTTTGTTTCTTGGAGTCCAC 276

Qy        403 TGCCGA---CAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTTGTCATCGAACAGGC 459
Db        277 TTCCAATTCCAAGAATGTGCCCCCAGACCTCTCCATCTGCACCTTTGTGCTGGAGCAGTC 336

Qy        460 GCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAAACTG------- 512
Db        337 CCTCTCTGTCCGGGCGCTGCAGGAGATGCTGGCTAACACCGTGGAGAAATCAGAAGGGCA 396

Qy        513 -----------------GGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTAC 555
Db        397 AGTTGATGTGGAAAAATGGAAATTCATGATGAAGACTGCTCAAGGTGGTGGTCATCGAAC 456

Qy        556 GCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTG 615
Db        457 ACTCCTCTACGGACATGCCATATTGCTGCGCCATTCCTATAGTGGCATGTATCTGTGCTG 516

Qy        616 CCTGTCAACATC---ATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCA 672
Db        517 CCTGTCCACCTCCCGGTCTTCAACTGATAAGCTGGCTTTTGATGTTGGCTTGCAAGAGGA 576

Qy        673 CTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGG 732
Db        577 CACCACAGGGGAGGCTTGTTGGTGGACCATACACCCTGCCTCTAAGCAGCGATCAGAAGG 636

Qy        733 CGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTT 792
Db        637 AGAAAAAGTACGAGTTGGAGATGACCTCATCTTAGTTAGCGTGTCCTCTGAAAGGTACTT 696

Qy        793 GCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCACTG 852
Db        697 GCACTTGTCTTATGGCAACGGCAGCTTACACGTGGATGCCGCTTTCCAGCAGACTCTCTG 756

Qy        853 GTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTCGG 912
Db        757 GAGCGTGGCCCCAATCAGCTCAGG------AAGTGAGGCAGCCCAAGGGTATCTCATTGG 810

Qy        913 AGGTGATGTGCTCAGGTTCTTCCATGGA---GGTGACGAGTGTCTCACTATACCTAGCAC 969
Db        811 TGGTGATGTCCTCAGGTTGCTGCATGGACACATGGACGAGTGTCTCACTGTCCCTTCAGG 870

Qy        970 TTGGACAAAGGATGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCA 1029
Db        871 AGAACATGGTGAAGAGCAGCGGAGAACTGTTCATTATGAAGGTGGCGCTGTGTCTGTTCA 930

Qy       1030 AGCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAA 1089
Db        931 TGCACGTTCCCTTTGGAGACTAGAGACGCTAAGAGTTGCGTGGAGTGGAAGCCACATAAG 990

Qy       1090 CTGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGA 1149
Db        991 ATGGGGACAGCCATTCCGACTACGCCATGTCACAACAGGAAAATACTTGAGTCTCATGGA 1050

Qy       1150 CCAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTG 1209
Db       1051 AGACAAAAACCTTCTACTCATGGACAAAGAGAAAGCTGATGTAAAATCAACAGCATTTAC 1110

Qy       1210 CCTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCAT 1269
Db       1111 CTTCCGGTCTTCCAAGGAAAAATTGGATGTAGGGGTGAGA---AAAGAAGTAGATGGCAT 1167

Qy       1270 AGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGG 1329
Db       1168 GGGAACATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGACACAGG 1227

Qy       1330 CTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGA 1389
Db       1228 CCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATACAACG 1287

Qy       1390 GAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTC 1449
Db       1288 TAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCGAGATC 1344

Qy       1450 ACAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAA 1509
Db       1345 CCAGCATGAAGAATCACGCACAGCCCGAGTTATCCGGAGCACAGTCTTCCTTTTCAATAG 1404

Qy       1510 GTTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTC 1569
Db       1405 ATTTATAAGGGGCCTTGATGCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCGATTTGCC 1464

Qy       1570 AGTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCC 1629
Db       1465 TATAGAGTCCG------TAAGCCTAAGTCTGCAGGATCTCATTGGCTACTTCCACCCCCC 1518

Qy       1630 CGATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCA 1689
Db       1519 AGATGAGCATTTAGAGCATGAAGACAAACAGAACAGACTACGAGCCCTGAAGAATCGGCA 1578

Qy       1690 GGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAA 1749
Db       1579 AAATCTCTTCCAGGAAGAGGGAATGATCAACCTCGTGCTTGAGTGCATAGACCGTTTGCA 1638

Qy       1750 CGTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAG 1809
Db       1639 CGTCTACAGCAGTGCAGCACACTTTGCTGATGTTGCTGGGCGA---GAAGCAGGAGAGTC 1695

Qy       1810 CTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCA 1869
Db       1696 TTGGAAATCCATTCTGAATTCTCTGTATGAGTTGCTGGCGGCTCTAATTAGAGGAAATCG 1755

Qy       1870 CACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGG 1929
Db       1756 TAAAAACTGTGCTCAATTTTCTGGCTC------------CCTCGACTGGTTGATCAGCAG 1803

Qy       1930 CTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGA 1989
Db       1804 ATTGGAAAGACTGGAAGCTTCTTCAGGCATTCTGGAAGTTTTACACTGTGTTTTAGTAGA 1863

Qy       1990 CTCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATT 2049
Db       1864 AAGTCCAGAAGCTCTAAATATTATTAAAGAAGGACATATTAAATCTATTATCTCACTTTT 1923

Qy       2050 AGAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAA 2109
```

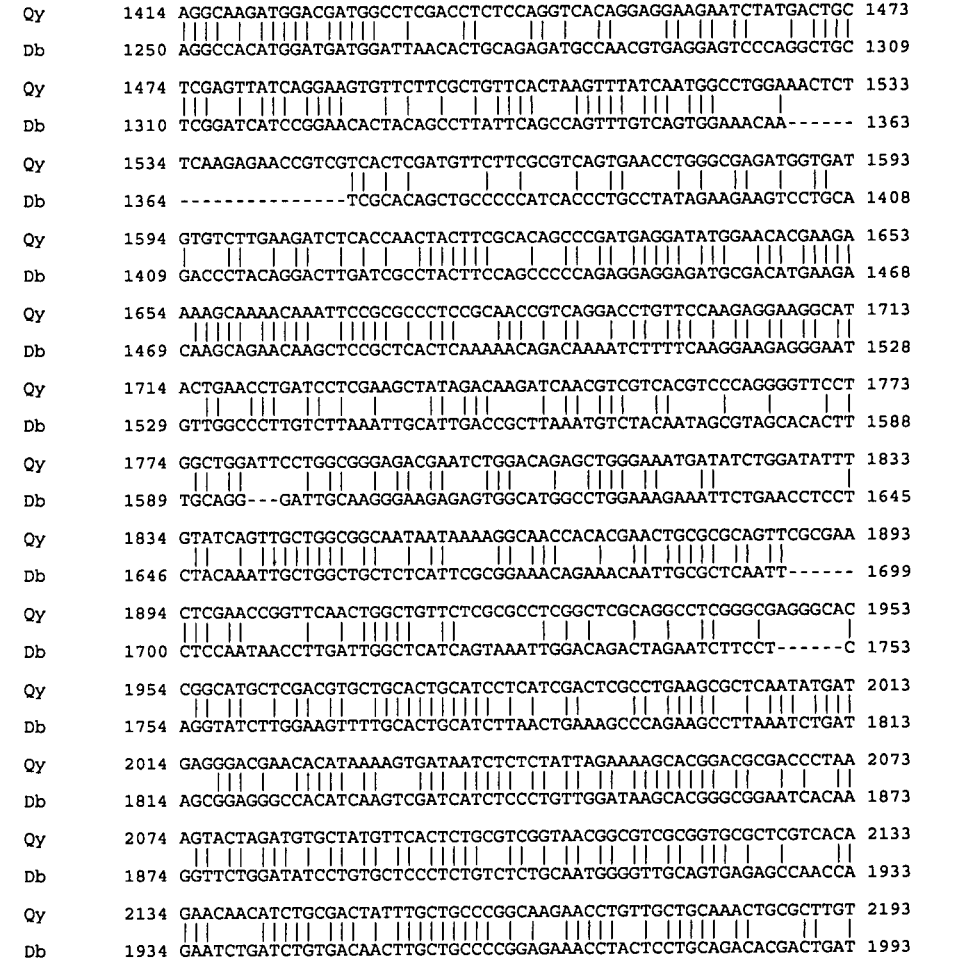


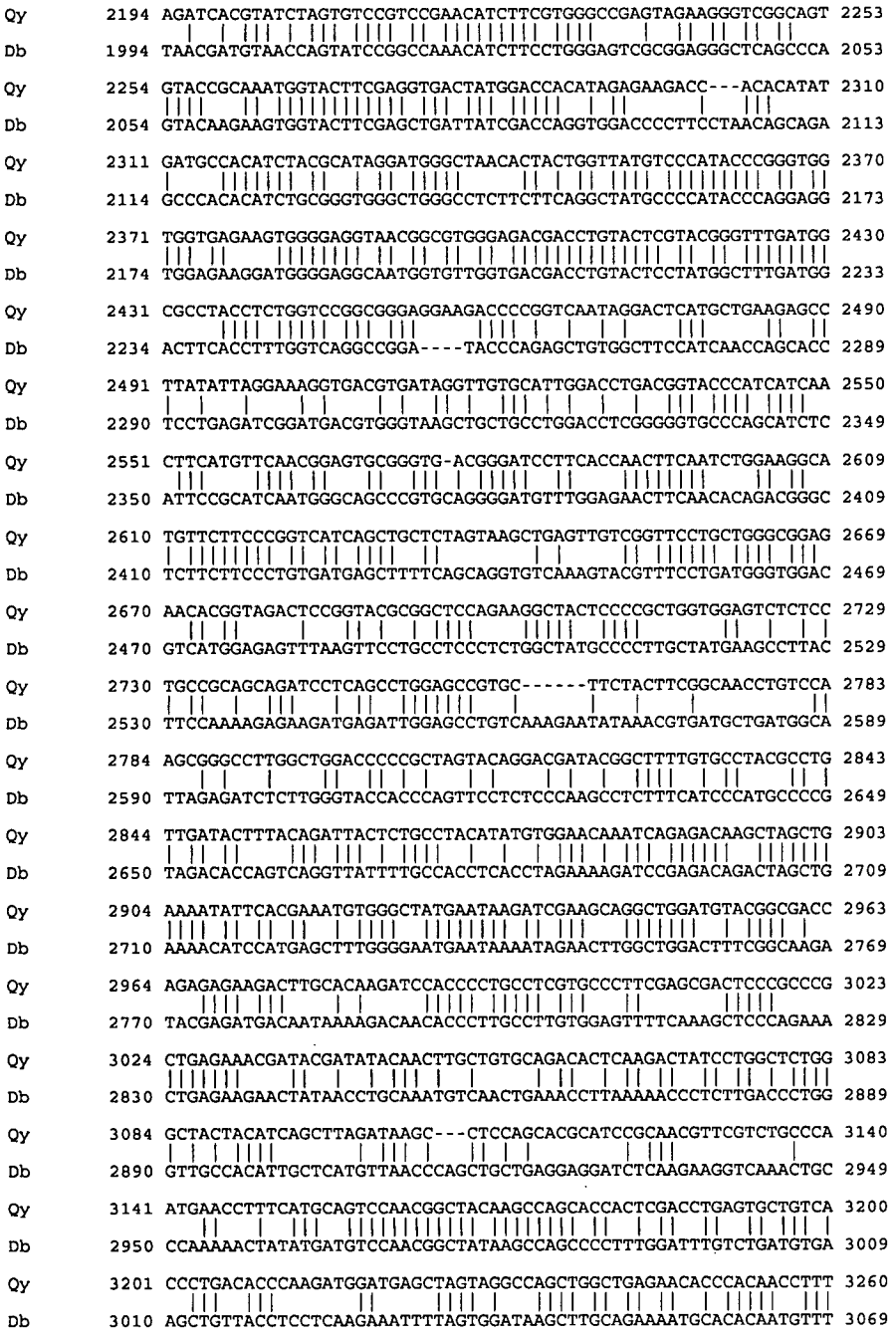


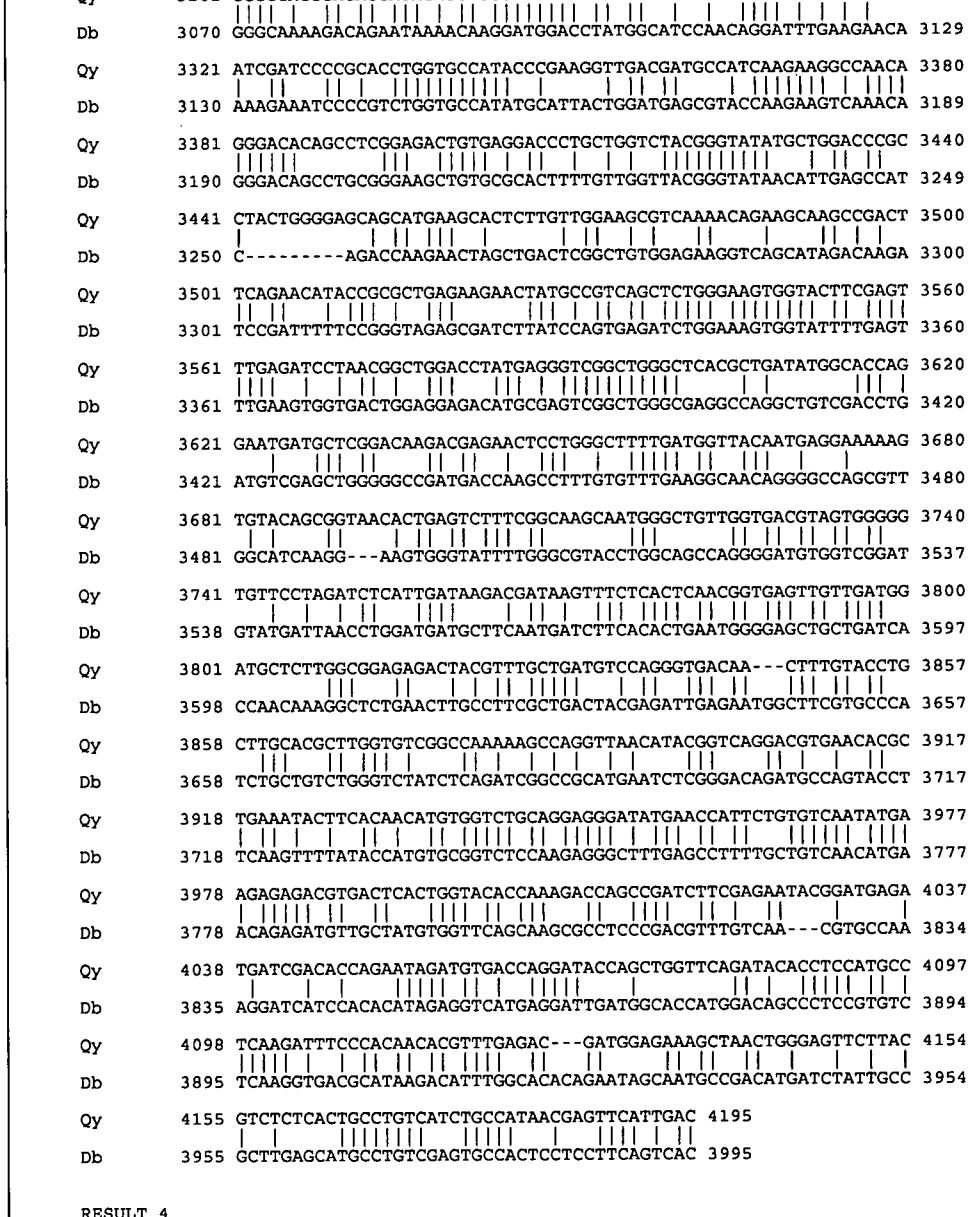
RESULT 3
US-09-424-783-1
; Sequence 1, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro

```
;  APPLICANT:  Nishimura, Seiichiro
;  APPLICANT:  Barsoumian, Edward Leon
;  TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
;  TITLE OF INVENTION:  and DNA Molecules Coding Therefor
;  FILE REFERENCE: 0652.2000000
;  CURRENT APPLICATION NUMBER: US/09/424,783
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/02926
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-424-783-1

  Query Match           16.2%;  Score 809;  DB 3;  Length 15572;
  Best Local Similarity   54.4%;  Pred. No. 4.5e-242;
  Matches 2112;  Conservative    0;  Mismatches 1665;  Indels  104;  Gaps   20;
```









RESULT 4
US-08-480-481-4
; Sequence 4, Application US/08480481
; Patent No. 5639614
; GENERAL INFORMATION:
; APPLICANT: Sen, Luyi
; APPLICANT: Philipson, Kenneth D.
; APPLICANT: Lusis, Aldons J.

```
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  380...380
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  776...776
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  1...1
;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  7987 of the rabbit cDNA homolog
US-08-480-481-4

  Query Match             1.3%;  Score 65.6;  DB 2;  Length 1050;
  Best Local Similarity   48.2%;  Pred. No. 2.8e-09;
  Matches  237;  Conservative    0;  Mismatches  234;  Indels   21;  Gaps    1;

Qy       2828 TTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATC 2887
              |||   ||    |||||||||||| | | | ||||   | |||    |  ||||| |  ||
Db        118 TTTAACCCACAACCTGTTGATACCTCAAATATTATAATTCCTGAGAAGTTGGAATACTTC 177

Qy       2888 AGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGC 2947
              |   ||||    || ||| ||  ||| || |  ||| | ||| | ||| | | |   ||
Db        178 ATTAACAAATATGCAGAACATTCTCATGACAAATGGTCAATGGACAAGTTAGCAAATGGA 237

Qy       2948 TGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTC 3007
              ||||| || || ||          |||||    |||||| || ||||    |    || |
Db        238 TGGATTTATGGAGAAATATATTCAGACTCCTCCAAGATTCAACCCTTGATGAAACCATAT 297

Qy       3008 GAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAG 3067
              | | | |  |       || |||  |    ||      |         |  | |||||

Db        298 AAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCTGGCCAATCAAAGAATCTCTCAAA 357

Qy       3068 ACTATCCTGGCTCTGGGCTACTACAT--------------------CAGCTTAGATAAG 3106
              |||||  |||||  |||| |   | ||                    |||| | |
Db        358 ACTATGTTGGCTTGGGGTTGGAAGATTGAAAGAACCCCAGAAGGAGACAGCATGGCCCTT 417

Qy       3107 CCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGC 3166
                |     |       || |    ||        | | |   || |         || | ||
Db        418 TATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGGTTTCTGTAGATGCTGCCCATGGT 477

Qy       3167 TACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTA 3226
              || |  ||   | |  | ||| ||||   ||| || ||   |     |  || |||   |
Db        478 TATAGTCCCCGAGCCATTGACATGAGCAATGTTACACTATCCAGAGACCTGCATGCTATG 537

Qy       3227 GTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGA 3286
              | ||    | ||||||| |||   || ||| | ||||| | | | | || || | ||
Db        538 GCAGAAATGATGGCTGAAAACTATCATAACATATGGGCAAAGAAAAAGAAACTGGAGTTG 597

Qy       3287 TGGACTTACGGA 3298
                | || | |||
Db        598 GAGTCTAAAGGA 609


RESULT 5
US-08-480-481-3
; Sequence 3, Application US/08480481
; Patent No. 5639614
;  GENERAL INFORMATION:
;    APPLICANT:  Sen, Luyi
;    APPLICANT:  Philipson, Kenneth D.
;    APPLICANT:  Lusis, Aldons J.
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
```

```
;      LOCATION:  1...1
;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  7987 of the rabbit cDNA homolog
US-08-480-481-3

  Query Match             1.3%;  Score 64;  DB 2;  Length 1050;
  Best Local Similarity   48.0%;  Pred. No. 8.9e-09;
  Matches  236;  Conservative    0;  Mismatches  235;  Indels   21;  Gaps    1;

Qy       2828 TTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATC 2887
              |||   ||    |||||||||| | | ||||   | |||    |  ||||| |  ||
Db        118 TTTAACCCACAACCTGTTGATACCTCAAATATTATAATTCCTGAGAAGTTGGAATACTTC 177

Qy       2888 AGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGC 2947
              |   ||||    || ||| ||  ||| || |  ||| | ||| | ||| | | |   ||
Db        178 ATTAACAAATATGCAGAACATTCTCATGACAAATGGTCAATGGACAAGTTAGCAAATGGA 237

Qy       2948 TGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTC 3007
              ||||| || || ||       |||||    |||||| || ||||   |    || |
Db        238 TGGATTTATGGAGAAATATATTCAGACTCCTCCAAGATTCAACCCTTGATGAAACCATAT 297

Qy       3008 GAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAG 3067
              | | | |       || ||| |    ||       |          |  | |||||
Db        298 AAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCTGGCCAATCAAAGAATCTCTCAAA 357

Qy       3068 ACTATCCTGGCTCTGGGCTACTACAT--------------------CAGCTTAGATAAG 3106
              |||||  |||||  ||| |    ||                    |||| | |
Db        358 ACTATGTTGGCTTGGGGTTGGAGGATTGAAAGAACCCCAGAAGGAGACAGCATGGCCCTT 417

Qy       3107 CCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGC 3166
                |     |      || |    ||       | | |   || |        || | ||
Db        418 TATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGGTTTCTGTAGATGCTGCCCATGGT 477

Qy       3167 TACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTA 3226
              || |  ||   | | | ||| ||||   ||| || ||  |      |  || |||   |
Db        478 TATAGTCCCCGAGCCATTGACATGAGCAATGTTACACTATCCAGAGACCTGCATGCTATG 537

Qy       3227 GTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGA 3286
              | ||    | ||||||| |||    || ||| | ||||| | | | | || || | ||
Db        538 GCAGAAATGATGGCTGAAAACTATCATAACATATGGGCAAAGAAAAAGAAACTGGAGTTG 597

Qy       3287 TGGACTTACGGA 3298
                | || | |||
Db        598 GAGTCTAAAGGA 609


RESULT 6
US-08-785-420-3
; Sequence 3, Application US/08785420
; Patent No. 6001976
;  GENERAL INFORMATION:
;    APPLICANT:  MacLennan, David H
;    APPLICANT:  O'Brien, Peter J.
;    TITLE OF INVENTION:  DIAGNOSIS FOR PORCINE MALIGNANT
;    TITLE OF INVENTION:  HYPERTHERMIA
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte,
;      STATE:  No. 6001976th Carolina 28234
;      COUNTRY:  U.S.A.
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,420
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,388
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/030,159
;      FILING DATE:  15-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Layton,Jr., Samuel G.
;      REGISTRATION NUMBER:  22807
;      REFERENCE/DOCKET NUMBER:  3477-73
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-377-1561
;      TELEFAX:  704-334-2014
;      TELEX:  57-5102
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1598 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Pig RYR1 gene
;    POSITION IN GENOME:
;      UNITS:  bp
US-08-785-420-3

  Query Match             1.1%;  Score 53.6;  DB 3;  Length 1598;
  Best Local Similarity   57.0%;  Pred. No. 2.2e-05;
  Matches   98;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy       2066 GACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGCGTCGCGGTGCGC 2125
              |||||  | || || ||||| || ||||| || || ||  | || || || || ||||||
Db        936 GACCCCTAGGTGCTGGATGTCCTGTGTTCCCTGTGTGTGTGCAATGGTGTGGCCGTGCGC 995

Qy       2126 TCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCTGTTGCTGCAAACT 2185
              ||    ||  |   |||    ||  | ||||| || |||    | ||  |||||| ||
Db        996 TCCAACCAAGATCTCATTACTGAGAACTTGCTCCCTGGCCGCGAGCTTCTGCTGCAGACA 1055

Qy       2186 GCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGCCGAG 2237
                || |  |  | ||  | ||     | ||    | ||| |    | |||
Db       1056 AACCTCATCAACTATGTCACCAGGTCTGGCCCCCCAACCTTTGACCCCAGAG 1107


RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
```

```
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.0%;  Score 51.6;  DB 2;  Length 7218;
  Best Local Similarity   5.7%;  Pred. No. 0.00029;
  Matches   24;  Conservative  222;  Mismatches  176;  Indels    0;  Gaps    0;

Qy       4194 ACGAGGCAGAAAAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGA 4253
              ||:::: :::::::::  ::: :  ::: :::::  :::::  :  :: :::    :: ::
Db       1436 ACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1377

Qy       4254 AAGAGGCAGTTGAAGCTCAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCA 4313
              :::::: ::  ::::   ::: :   :   : :  ::  :::  : :::::: ::    :
Db       1376 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1317

Qy       4314 CCATGAACGATATTAAAGGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCA 4373
                : ::: :: :  :::::   : :  : ::::: ::  :::::::::  :   ::    :
Db       1316 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1257

Qy       4374 AGATGAAGCGCCTGCCTTCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTA 4433
              ::: :::: :   :   :::: :  : : :::::   : :: :::::: :  :  :
Db       1256 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1197

Qy       4434 TACAAAATTACAATAATTTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTG 4493
              : ::::  : :: ::   : ::  ::: :::  :: :: : : :  ::  ::  :: :
Db       1196 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1137

Qy       4494 AAGCTGAAATGGCCAAGTATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGG 4553
              :::  :::: ::  ::: : ::   ::::: : ::::   :: :   :: :: :::::::
Db       1136 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1077

Qy       4554 ACAAGAGGGGACGATCGCCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATC 4613
              : :::::::::|          ||  |  |  || |||       ||     ||  | |||| |
Db       1076 RRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGGAATTAATTCTGTGAGC 1017

Qy       4614 GT 4615
              ||
Db       1016 GT 1015


RESULT 8
US-08-480-481-6
; Sequence 6, Application US/08480481
; Patent No. 5639614
;  GENERAL INFORMATION:
;    APPLICANT:  Sen, Luyi
;    APPLICANT:  Philipson, Kenneth D.
;    APPLICANT:  Lusis, Aldons J.
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...1
;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  8137 of the rabbit cDNA homolog
;      NAME/KEY:  Other
;      LOCATION:  230...230
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  626...626
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
US-08-480-481-6

  Query Match             1.0%;  Score 51;  DB 2;  Length 900;
  Best Local Similarity   47.0%;  Pred. No. 9.6e-05;
  Matches  214;  Conservative    0;  Mismatches  220;  Indels   21;  Gaps    1;

Qy       2865 TGCCTACATATGTGGAACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGG 2924
              | |||     |  ||||| |  |||   ||||    || ||| ||  ||| || |  |||
Db          5 TTCCTGAGAAGTTGGAATACTTCATTAACAAATATGCAGAACATTCTCATGACAAATGGT 64

Qy       2925 CTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGA 2984
              | ||| | ||| | | |   || ||||| || || ||          |||||    |||||
Db         65 CAATGGACAAGTTAGCAAATGGATGGATTTATGGAGAAATATATTCAGACTCCTCCAAGA 124

Qy       2985 TCCACCCCTGCCTCGTGCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATAC 3044
              | || ||||   |    || |   | | | |  |        || |||  |    ||
Db         125 TTCAACCCTTGATGAAACCATATAAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCT 184

Qy       3045 AACTTGCTGTGCAGACACTCAAGACTATCCTGGCTCTGGGCTACTACAT---------- 3093
                |          | | ||||| |||||  |||||  ||| |   | ||
Db         185 GGCCAATCAAAGAATCTCTCAAAACTATGTTGGCTTGGGGTTGGAAGATTGAAAGAACCC 244

Qy       3094 ----------CAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAATG 3143
                       |||| | |      |      ||  |    ||       | | |
Db         245 CAGAAGGAGACAGCATGGCCCTTTATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGG 304

Qy       3144 AACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCC 3203
                || |         || | || || |  ||   | |  | ||| ||||   ||| || |
```

```
Db        305 TTTCTGTAGATGCTGCCCATGGTTATAGTCCCCGAGCCATTGACATGAGCAATGTTACAC 364

Qy       3204 TGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGG 3263

Db        365 TATCCAGAGACCTGCATGCTATGGCAGAAATGATGGCTGAAAACTATCATAACATATGGG 424

Qy       3264 CCAGGGAGAGGATACAGCAGGGATGGACTTACGGA 3298

Db        425 CAAAGAAAAAGAAACTGGAGTTGGAGTCTAAAGGA 459


RESULT 9
US-09-668-097A-35
; Sequence 35, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Edgar B.
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Klein, Ted
;  APPLICANT:  Shen, Jennie
;  TITLE OF INVENTION: Plant Lipases
;  FILE REFERENCE: BB1401 US NA
;  CURRENT APPLICATION NUMBER: US/09/668,097A
;  CURRENT FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER: 60/157309
;  PRIOR FILING DATE: 1999-10-01
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
;   LENGTH: 1334
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-668-097A-35

  Query Match             0.8%;  Score 40.8;  DB 3;  Length 1334;
  Best Local Similarity   58.1%;  Pred. No. 0.21;
  Matches   72;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy       1864 CAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCG 1923

Db        728 CAACGCCGGCGACTACGACCAGTACGGCTGCCTGAAGCGGTTCAACGCGCTGTCGGCCCG 787

Qy       1924 CCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCT 1983

Db        788 CCACAACTCGCTGCTCCAGAGCAAGGTGACCAGCCTGCAGGGCAAGTACCCCTACGCCAA 847

Qy       1984 CATC 1987

Db        848 GATC 851


RESULT 10
US-09-252-991A-11838
; Sequence 11838, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11838
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11838

  Query Match             0.8%;  Score 39.4;  DB 3;  Length 294;
  Best Local Similarity   52.8%;  Pred. No. 0.19;
  Matches   85;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy       3280 GCAGGGATGGACTTACGGACTTAATGAGGACTCGGACATGCATCGATCCCCGCACCTGGT 3339

Db         84 GCAGCAGCAGCCCTACGGACCCAACCCGGACTCGAAATCGCTCCGCCAGCACTACGTGGA 143

Qy       3340 GCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGAC 3399

Db        144 AGGGCGCCTGGACATCGCCCGGGTGATCTACAAGACCGACCTGTGGAGCGCCTGTGGGAT 203

Qy       3400 TGTGAGGACCCTGCTGGTCTACGGGTATATGCTGGACCCGC 3440

Db        204 CGTCCCGGCGCGCCTGGTCTACGAGGACTCGCAGGGCGAGC 244


RESULT 11
US-09-485-529-13
; Sequence 13, Application US/09485529
; Patent No. 6762348
; GENERAL INFORMATION:
;  APPLICANT: Harberd, Nicholas P
;  APPLICANT:  Richards, Donald E
;  APPLICANT:  Peng, Jinrong
;  TITLE OF INVENTION: Genetic Control of Plant Growth and Development
;  FILE REFERENCE: 620-91
;  CURRENT APPLICATION NUMBER: US/09/485,529
;  CURRENT FILING DATE:  2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/GB98/02383
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: GB 9717192.0
;  PRIOR FILING DATE: 1997-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 1768
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-485-529-13

  Query Match             0.8%;  Score 38.6;  DB 3;  Length 1768;
  Best Local Similarity   47.6%;  Pred. No. 1.2;
  Matches  147;  Conservative    0;  Mismatches  159;  Indels    3;  Gaps    1;

Qy       1873 GAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTC 1932

Db         573 GAAGCTCGCCCAGTTCGCGCACACCATCCGCGTCGACTTCCAGTACCGCGGCCTCGTCGC 632

Qy       1933 GCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTC 1992

Db         633 ---CGCCACGCTCGCGGACCTGGAGCCGTTCATGCTGCAGCCGGAGGGCGAGGAGGACCC 689

Qy       1993 GCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGA 2052

Db         690 GAACGAGGAGCCCGAGGTAATCGCCGTCAACTCAGTCTTCGAGATGCACCGGCTGCTCGC 749

Qy       2053 AAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGG 2112

Db         750 GCAGCCCGGCGCCCTGGAGAAGGTCCTGGGCACCGTGCGCGCCGTGCGGCCCAGGATCGT 809

Qy       2113 CGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCT 2172

Db         810 CACCGTGGTGGAGCAGGAGGCGAATCACAACTCCGGCACATTCCTGGACCGCTTCACCGA 869

Qy       2173 GTTGCTGCA 2181

Db         870 GTCTCTGCA 878


RESULT 12
US-09-485-529-14
; Sequence 14, Application US/09485529
```

```
; Patent No. 6762348
; GENERAL INFORMATION:
;  APPLICANT: Harberd, Nicholas P
;  APPLICANT:  Richards, Donald E
;  APPLICANT:  Peng, Jinrong
;  TITLE OF INVENTION: Genetic Control of Plant Growth and Development
;  FILE REFERENCE: 620-91
;  CURRENT APPLICATION NUMBER: US/09/485,529
;  CURRENT FILING DATE:  2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/GB98/02383
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: GB 9717192.0
;  PRIOR FILING DATE: 1997-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;    LENGTH: 2125
;    TYPE: DNA
;    ORGANISM: Triticum aestivum
US-09-485-529-14

  Query Match             0.8%;  Score 38.6;  DB 3;  Length 2125;
  Best Local Similarity   47.6%;  Pred. No. 1.4;
  Matches  147;  Conservative    0;  Mismatches  159;  Indels    3;  Gaps    1;

Qy       1873 GAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTC 1932
              |||   ||| |||||||||| || | | |||  || |||  | || |    |||||| | |
Db       1194 GAAGCTCGCCCAGTTCGCGCACACCATCCGCGTCGACTTCCAGTACCGCGGCCTCGTCGC 1253

Qy       1933 GCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTC 1992
                 ||| ||  || || |   |    | ||    ||| ||       |      ||| |
Db       1254 ---CGCCACGCTCGCGGACCTGGAGCCGTTCATGCTGCAGCCGGAGGGCGAGGAAGACCC 1310

Qy       1993 GCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGA 2052
              |   || | || | |  | |||    | | |      |    | |||   |   ||  | |
Db       1311 GAACGAGGAGCCCGAGGTAATCGCCGTCAACTCAGTCTTCGAGATGCACCGGCTGCTCGC 1370

Qy       2053 AAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGG 2112
                |||  |||   |      || || || |      |  |  |  |  |   | | | ||
Db       1371 GCAGCCCGGCGCCCTGGAGAAGGTCCTGGGCACCGTGCGCGCCGTGCGGCCCAGGATCGT 1430

Qy       2113 CGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCT 2172
              |  || ||||      |      |||  ||| || || |   || |||  | ||   | |
Db       1431 CACCGTGGTGGAGCAGGAGGCGAATCACAACTCCGGCACATTCCTGGACCGCTTCACCGA 1490

Qy       2173 GTTGCTGCA 2181
              ||  |||||
Db       1491 GTCTCTGCA 1499


RESULT 13
US-09-902-540-5006
; Sequence 5006, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5006
;    LENGTH: 1290
;    TYPE: DNA
;    ORGANISM: Myxococcus xanthus
US-09-902-540-5006

  Query Match             0.8%;  Score 38.2;  DB 3;  Length 1290;
  Best Local Similarity   56.4%;  Pred. No. 1.3;
  Matches   92;  Conservative    0;  Mismatches   68;  Indels    3;  Gaps    1;

Qy       1864 CAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCG 1923
              |||||| |      |||||      ||  |||  | ||||| |    |  |||| || | |
Db        906 CAACCAGAACCTGAGCGCGTTCAGCGGCAACGAGTACCGGGTGGGCACGCTGCTCGCCAG 965

Qy       1924 CCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCT 1983
              |    ||  ||||||   ||||||| ||||||    | ||||||||||   ||  | |
Db        966 CGCGCTCTACCAGGCC---GGCGAGGCCACCGGTCAACGCGACGTGCTGCTGCGCGCCAT 1022

Qy       1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACAC 2026
              | ||| ||||    | |     |  | || || |  ||  | |
Db       1023 CGTCGCCTCGTACAACGACGAGAGCACGACGACGCCCGGGCTC 1065


RESULT 14
US-09-902-540-1036
; Sequence 1036, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1036
;    LENGTH: 12950
;    TYPE: DNA
;    ORGANISM: Myxococcus xanthus
;    FEATURE:
;    NAME/KEY: unsure
;    LOCATION: (1)..(12950)
;    OTHER INFORMATION: unsure at all n locations
US-09-902-540-1036

  Query Match             0.8%;  Score 38.2;  DB 3;  Length 12950;
  Best Local Similarity   56.4%;  Pred. No. 7.1;
  Matches   92;  Conservative    0;  Mismatches   68;  Indels    3;  Gaps    1;

Qy       1864 CAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCG 1923
              |||||| |      |||||      ||  |||  | ||||| |    |  |||| || | |
Db       1307 CAACCAGAACCTGAGCGCGTTCAGCGGCAACGAGTACCGGGTGGGCACGCTGCTCGCCAG 1366

Qy       1924 CCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCT 1983
              |    ||  ||||||   ||||||| ||||||    | ||||||||||   ||  | |
Db       1367 CGCGCTCTACCAGGCC---GGCGAGGCCACCGGTCAACGCGACGTGCTGCTGCGCGCCAT 1423

Qy       1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACAC 2026
              | ||| ||||    | |     |  | || || |  ||  | |
Db       1424 CGTCGCCTCGTACAACGACGAGAGCACGACGACGCCCGGGCTC 1466


RESULT 15
US-09-621-976-8976
; Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
```

; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match 0.8%; Score 37.8; DB 3; Length 399;
Best Local Similarity 10.5%; Pred. No. 0.75;
Matches 24; Conservative 114; Mismatches 91; Indels 0; Gaps 0;

```
Qy       4116 CGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTCTTACGTCTCTCACTGCCTGTCATCT 4175
             ::: ::|::: ::::::::::   ::     :::   :: ::  :| :::|       | :
Db         30 SKKSWRAKMSWMKKRRRRRRAWMWWKSMCWMKKSKSWWRSWGMMTKRMKGRGAASWAGYM 89

Qy       4176 GCCATAACGAGTTCATTGACGAGGCAGAAAAAGCCAGGCGTTGGGTAGAAATCAAGGACC 4235
             : : ::  :::::   ::||   : ||::  ||  :  : :     ::: |   :  : :
Db         90 SWMTYMTRRWRYYRYRKKACTKWRAAGMWGKAGWAWMAYAKMWYMAWRRTAMKYWAMMKS 149

Qy       4236 GCCAACGGATCCTAATGAAAGAGGCAGTTGAAGCTCAGATGTCCGCCCATATTGACCAGA 4295
             : ::: ::|:: :: : :|::    ::     :| ::|:|  ::  :::: : : :::||:
Db        150 KRSMRRRRAWYAWMYYMMARRTMWGMRASCYRGAYMASAGMYYWMMYYMMRRKWMYSAGW 209

Qy       4296 TCATGAGGAGCGGTTTCACCATGAACGATATTAAAGGTTTGCACTACGA 4344
              :: :: ::  :   :: :|::|| : ::::| ::: :: :::|| :::
Db        210 SMMRKWTRRCASYSCWSSYCMWGAKMMMYWKTSRWSYWYSSYRCTKYRR 258
```

Search completed: October 10, 2006, 16:25:34
Job time : 866 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: October 10, 2006, 15:44:20 ; Search time 3799 Seconds
(without alignments)
16172.197 Million cell updates/sec

Title: US-10-668-767-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 ctaaattcgaaattcccatc.....ggtgaccacccagtaccact 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

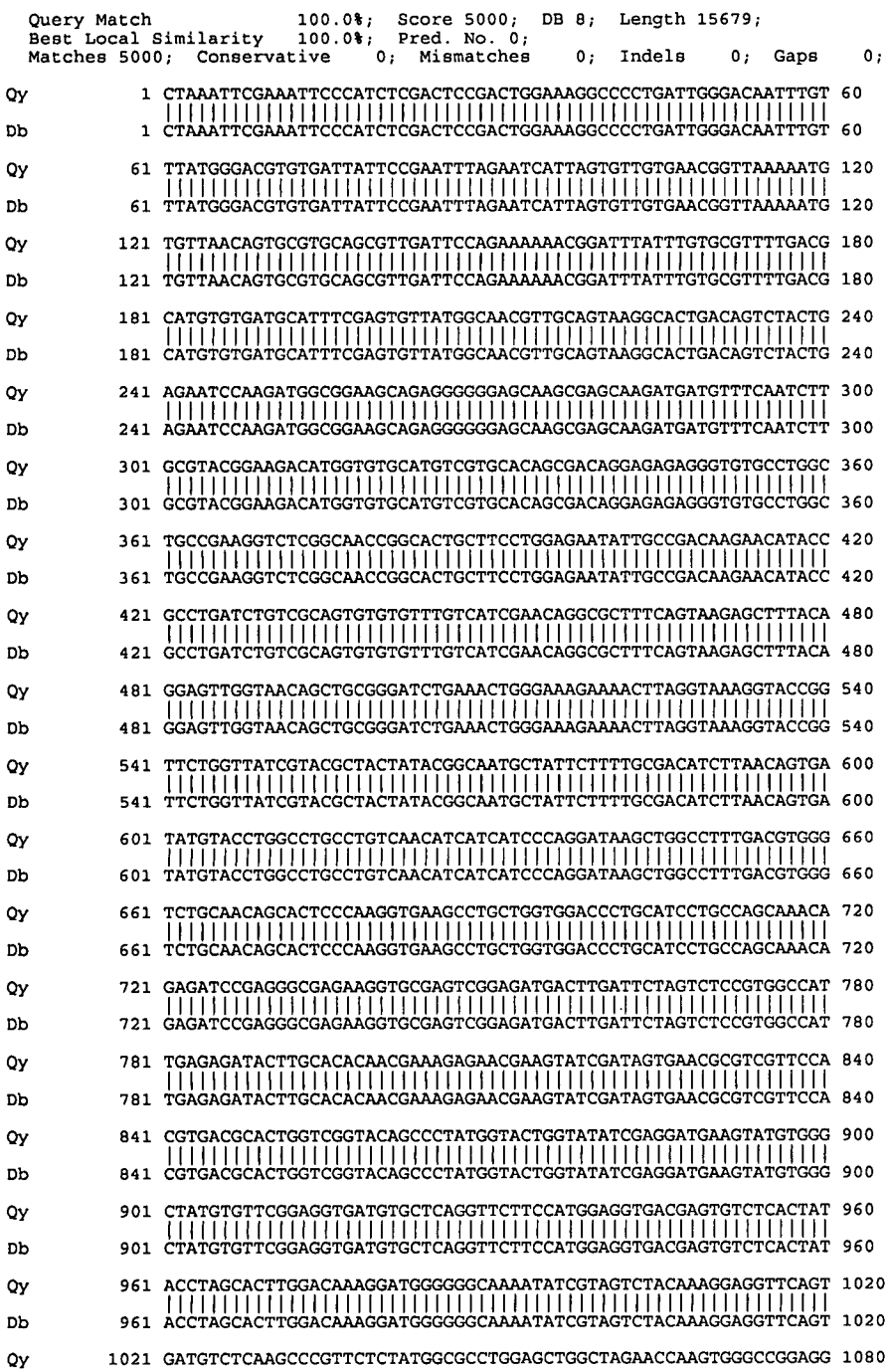
SUMMARIES

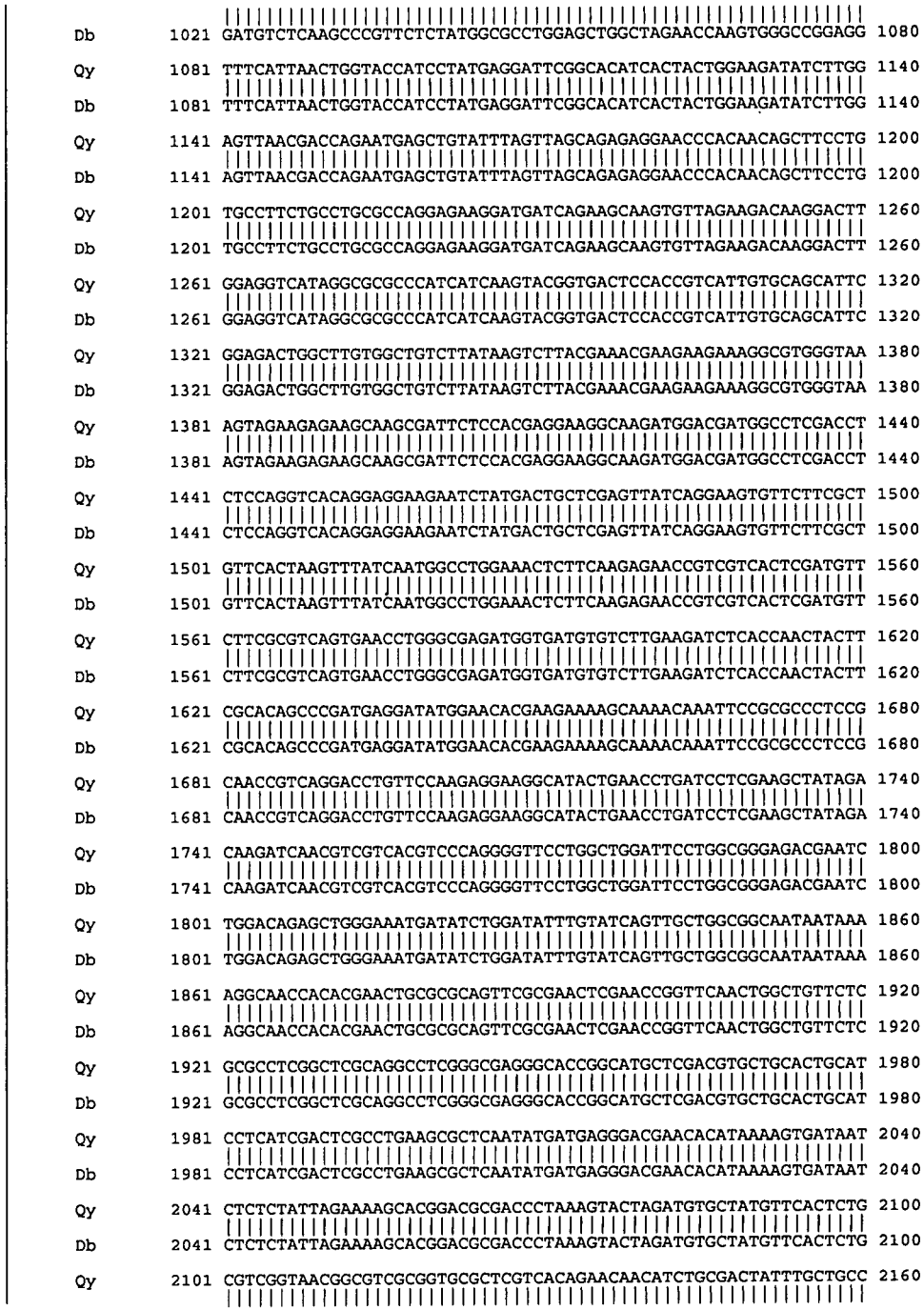
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5000	100.0	15679	8	US-10-668-767-1	Sequence 1, Appli
	2	4570.8	91.4	15429	8	US-10-668-767-143	Sequence 143, App
	3	4501.6	90.0	15405	8	US-10-668-767-129	Sequence 129, App
	4	4472.8	89.5	15387	8	US-10-668-767-127	Sequence 127, App
	5	4288.8	85.8	15303	8	US-10-668-767-145	Sequence 145, App
	6	2185.8	43.7	16363	8	US-10-668-767-9	Sequence 9, Appli
	7	2158.2	43.2	15606	13	US-11-097-143-22562	Sequence 22562, A
	8	2078.2	41.6	15413	8	US-10-668-767-7	Sequence 7, Appli
	9	1846	36.9	15845	8	US-10-668-767-3	Sequence 3, Appli
	10	1835.2	36.7	15315	8	US-10-668-767-5	Sequence 5, Appli
c	11	1455.8	29.1	24236	13	US-11-097-143-22561	Sequence 22561, A
	12	840.8	16.8	4078	7	US-10-305-720-1154	Sequence 1154, Ap
	13	840.8	16.8	14302	8	US-10-276-774-552	Sequence 552, App
	14	840.8	16.8	15731	10	US-10-887-553A-490	Sequence 490, App
	15	831.4	16.6	15359	8	US-10-276-774-500	Sequence 500, App
	16	831.4	16.6	15359	10	US-10-887-553A-489	Sequence 489, App
	17	831.4	16.6	15359	10	US-10-450-763-4960	Sequence 4960, Ap
	18	821.4	16.4	15563	8	US-10-764-425-48	Sequence 48, Appl
	19	821.4	16.4	15563	10	US-10-887-553A-491	Sequence 491, App
	20	821.4	16.4	15564	15	US-11-000-688-1500	Sequence 1500, Ap
	21	809	16.2	15583	10	US-10-450-763-12305	Sequence 12305, A
	22	809	16.2	15820	10	US-10-450-763-23337	Sequence 23337, A
	23	801.2	16.0	15453	9	US-10-723-860-5796	Sequence 5796, Ap
	24	712.2	14.2	14620	15	US-11-044-111-17	Sequence 17, Appl
	25	686.8	13.7	3168	15	US-11-044-111-8	Sequence 8, Appli
	26	151	3.0	717	15	US-11-044-111-18	Sequence 18, Appl
	27	130.6	2.6	636	15	US-11-044-111-19	Sequence 19, Appl
	28	106.4	2.1	321	7	US-10-029-386-16105	Sequence 16105, A
	29	106.4	2.1	597	7	US-10-029-386-2405	Sequence 2405, Ap
	30	90.2	1.8	524	15	US-11-044-111-20	Sequence 20, Appl
	31	86.4	1.7	479	12	US-10-301-480-3997	Sequence 3997, Ap
	32	86.4	1.7	479	12	US-10-301-480-617406	Sequence 617406,
c	33	86.4	1.7	535	6	US-10-027-632-59310	Sequence 59310, A
c	34	86.4	1.7	535	7	US-10-027-632-59310	Sequence 59310, A
c	35	86.4	1.7	643	6	US-10-027-632-51124	Sequence 51124, A
c	36	86.4	1.7	643	7	US-10-027-632-51124	Sequence 51124, A
	37	84.6	1.7	1800	10	US-10-450-763-23334	Sequence 23334, A
	38	71.6	1.4	595	12	US-10-301-480-261241	Sequence 261241,
	39	71.6	1.4	595	12	US-10-301-480-261242	Sequence 261242,
	40	71.6	1.4	595	12	US-10-301-480-874650	Sequence 874650,
	41	71.6	1.4	595	12	US-10-301-480-874651	Sequence 874651,
c	42	71.6	1.4	608	4	US-09-925-065A-169264	Sequence 169264,
c	43	71.6	1.4	608	4	US-09-925-065A-169265	Sequence 169265,
c	44	71.6	1.4	608	5	US-09-925-065A-169264	Sequence 169264,
c	45	71.6	1.4	608	5	US-09-925-065A-169265	Sequence 169265,

ALIGNMENTS

RESULT 1
US-10-668-767-1
; Sequence 1, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15679
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)..(15676)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5515)
; OTHER INFORMATION: n = c or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13000)
; OTHER INFORMATION: n = a or t
US-10-668-767-1

Query Match 100.0%; Score 5000; DB 8; Length 15679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



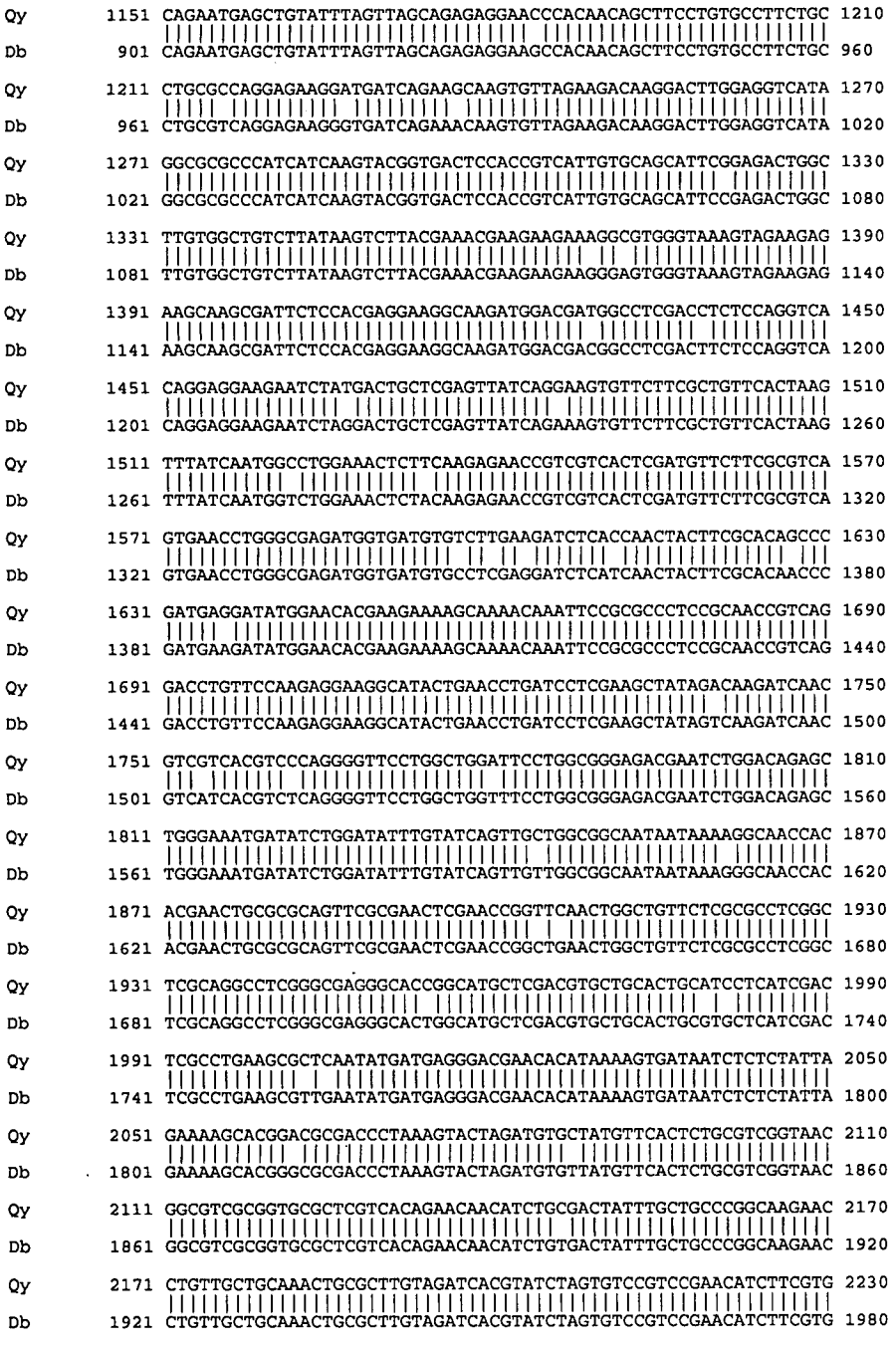


```
Db      2101 CGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCC 2160
Qy      2161 CGGCAAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAA 2220
Db      2161 CGGCAAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAA 2220
Qy      2221 CATCTTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGAC 2280
Db      2221 CATCTTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGAC 2280
Qy      2281 TATGGACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAA 2340
Db      2281 TATGGACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAA 2340
Qy      2341 CACTACTGGTTATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGG 2400
Db      2341 CACTACTGGTTATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGG 2400
Qy      2401 AGACGACCTGTACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGAC 2460
Db      2401 AGACGACCTGTACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGAC 2460
Qy      2461 CCCGGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTG 2520
Db      2461 CCCGGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTG 2520
Qy      2521 TGCATTGGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGG 2580
Db      2521 TGCATTGGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGG 2580
Qy      2581 ATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAA 2640
Db      2581 ATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAA 2640
Qy      2641 GCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGA 2700
Db      2641 GCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGA 2700
Qy      2701 AGGCTACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTG 2760
Db      2701 AGGCTACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTG 2760
Qy      2761 CTTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGA 2820
Db      2761 CTTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGA 2820
Qy      2821 TACGGCTTTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGA 2880
Db      2821 TACGGCTTTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGA 2880
Qy      2881 ACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGA 2940
Db      2881 ACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGA 2940
Qy      2941 AGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGT 3000
Db      2941 AGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGT 3000
Qy      3001 GCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGAC 3060
Db      3001 GCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGAC 3060
Qy      3061 ACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCAT 3120
Db      3061 ACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCAT 3120
Qy      3121 CCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACC 3180
Db      3121 CCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACC 3180
Qy      3181 ACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGC 3240
Db      3181 ACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGC 3240
```

```
Qy      3241 TGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACT 3300
Db      3241 TGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACT 3300
Qy      3301 TAATGAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGA 3360
Db      3301 TAATGAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGA 3360
Qy      3361 TGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTA 3420
Db      3361 TGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTA 3420
Qy      3421 CGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTC 3480
Db      3421 CGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTC 3480
Qy      3481 AAAACAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTC 3540
Db      3481 AAAACAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTC 3540
Qy      3541 TGGGAAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGC 3600
Db      3541 TGGGAAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGC 3600
Qy      3601 TCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGA 3660
Db      3601 TCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGA 3660
Qy      3661 TGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGC 3720
Db      3661 TGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGC 3720
Qy      3721 TGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACT 3780
Db      3721 TGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACT 3780
Qy      3781 CAACGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGG 3840
Db      3781 CAACGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGG 3840
Qy      3841 TGACAACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGG 3900
Db      3841 TGACAACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGG 3900
Qy      3901 TCAGGACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACC 3960
Db      3901 TCAGGACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACC 3960
Qy      3961 ATTCTGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTT 4020
Db      3961 ATTCTGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTT 4020
Qy      4021 CGAGAATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTC 4080
Db      4021 CGAGAATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTC 4080
Qy      4081 AGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAA 4140
Db      4081 AGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAA 4140
Qy      4141 CTGGGAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGC 4200
Db      4141 CTGGGAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGC 4200
Qy      4201 AGAAAAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGC 4260
Db      4201 AGAAAAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGC 4260
Qy      4261 AGTTGAAGCTCAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAA 4320
Db      4261 AGTTGAAGCTCAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAA 4320
```

```
Qy       4321 CGATATTAAAGGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CGATATTAAAGGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAA 4380

Qy       4381 GCGCCTGCCTTCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 GCGCCTGCCTTCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAA 4440

Qy       4441 TTACAATAATTTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 TTACAATAATTTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGA 4500

Qy       4501 AATGGCCAAGTATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAG 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 AATGGCCAAGTATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAG 4560

Qy       4561 GGGACGATCGCCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GGGACGATCGCCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAA 4620

Qy       4621 ATCCCGTAAATCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATCCCGTAAATCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGG 4680

Qy       4681 TGCTCGAAGGCCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCAT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCTCGAAGGCCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCAT 4740

Qy       4741 GAACGCGCGTCCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAACGCGCGTCCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGC 4800

Qy       4801 TCAGATGGCGACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTC 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TCAGATGGCGACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTC 4860

Qy       4861 GGCTACGGAAACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGA 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGCTACGGAAACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGA 4920

Qy       4921 GTACTTTTATGGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GTACTTTTATGGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTG 4980

Qy       4981 GGTGACCACCCAGTACCACT 5000
             ||||||||||||||||||||
Db       4981 GGTGACCACCCAGTACCACT 5000
```

```
RESULT 2
US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
;   LENGTH: 15429
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15429)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv3
US-10-668-767-143

  Query Match             91.4%;  Score 4570.8;  DB 8;  Length 15429;
  Best Local Similarity   97.6%;  Pred. No. 0;
  Matches 4638;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy        251 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAA 310
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCATTCTTGCGTACGGAA 60

Qy        311 GACATGGTGTGCATGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 370
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATGGTGTGCCTGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 120

Qy        371 CTCGGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTG 430
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 TTCGGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCACCTGATCTG 180

Qy        431 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 240

Qy        491 ACAGCTGCGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTAT 550
              || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||
Db        241 ACGGCTGCGGGTTCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTCAT 300

Qy        551 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 360

Qy        611 GCCTGCCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 670
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTGCCTGTCGACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 420

Qy        671 CACTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 730
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTCCCAGGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 480

Qy        731 GGCGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATAC 790
              || |||||||||||||||||||||||||||||||| |||||||||| | ||||||||||
Db        481 GGTGAGAAGGTGCGAGTCGGAGATGACTTGATTCTGGTCTCCGTGGCTACTGAGAGATAC 540

Qy        791 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCAC 850
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        541 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACCCAC 600

Qy        851 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTC 910
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        601 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTAGGCTATGTGTTC 660

Qy        911 GGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACT 970
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||| ||
Db        661 GGAGGTGATGTGCTGCGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGTACC 720

Qy        971 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAA 1030
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        721 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACGAAGGAGGTTCAGTGATGTCTCAA 780

Qy       1031 GCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 1090
              ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCCGGTCTTTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 840

Qy       1091 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGAC 1150
              |||||||| |||||||||||||||||||||||||||||||||||| ||||| ||||||
Db        841 TGGTACCACCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTCGGAGTAAACGAC 900
```


Qy 1151 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGC 1210
Db 901 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAAGCCACAACAGCTTCCTGTGCCTTCTGC 960
Qy 1211 CTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1270
Db 961 CTGCGTCAGGAGAAGGGTGATCAGAAACAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1020
Qy 1271 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGC 1330
Db 1021 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACTGGC 1080
Qy 1331 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAG 1390
Db 1081 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAAGAG 1140
Qy 1391 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCA 1450
Db 1141 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGACGGCCTCGACTTCTCCAGGTCA 1200
Qy 1451 CAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAG 1510
Db 1201 CAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGAAAGTGTTCTTCGCTGTTCACTAAG 1260
Qy 1511 TTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1570
Db 1261 TTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1320
Qy 1571 GTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCC 1630
Db 1321 GTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAACCC 1380
Qy 1631 GATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAG 1690
Db 1381 GATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAG 1440
Qy 1691 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAC 1750
Db 1441 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGTCAAGATCAAC 1500
Qy 1751 GTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGC 1810
Db 1501 GTCATCACGTCTCAGGGGTTCCTGGCTGGTTTCCTGGCGGGAGACGAATCTGGACAGAGC 1560
Qy 1811 TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCAC 1870
Db 1561 TGGGAAATGATATCTGGATATTTGTATCAGTTGTTGGCGGCAATAATAAAGGGCAACCAC 1620
Qy 1871 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGC 1930
Db 1621 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTGAACTGGCTGTTCTCGCGCCTCGGC 1680
Qy 1931 TCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGAC 1990
Db 1681 TCGCAGGCCTCGGGCGAGGGCACTGGCATGCTCGACGTGCTGCACTGCGTGCTCATCGAC 1740
Qy 1991 TCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 2050
Db 1741 TCGCCTGAAGCGTTGAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 1800
Qy 2051 GAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAAC 2110
Db 1801 GAAAAGCACGGGCGCGACCCTAAAGTACTAGATGTGTTATGTTCACTCTGCGTCGGTAAC 1860
Qy 2111 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAAC 2170
Db 1861 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTATTTGCTGCCCGGCAAGAAC 1920
Qy 2171 CTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 2230
Db 1921 CTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 1980
Qy 2231 GGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCAC 2290
Db 1981 GGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAAGTGACTATGGACCAC 2040
Qy 2291 ATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGT 2350
Db 2041 ATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGC 2100
Qy 2351 TATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTG 2410
Db 2101 TACGTCCCATACCCGGGTGGTGGTGAAAAGTGGGGAGGTAACGGCGTGGGAGACGACCTG 2160
Qy 2411 TACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAAT 2470
Db 2161 TACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAAACTCCCGTCAAT 2220
Qy 2471 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGAC 2530
Db 2221 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCGTTAGAC 2280
Qy 2531 CTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2590
Db 2281 CTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2340
Qy 2591 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGT 2650
Db 2341 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAATTGAGTTGC 2400
Qy 2651 CGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCC 2710
Db 2401 CGGTTCCTGCTGGGCGGGGAACATGGTAGACTCCGGCACGCGGCTCCAGAAGGCTACTCC 2460
Qy 2711 CCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTC 2770
Db 2461 CCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCTTGCTTCTACTTC 2520
Qy 2771 GGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTT 2830
Db 2521 GGCAACCTGTCCAAGCGCGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTT 2580
Qy 2831 GTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGA 2890
Db 2581 GTGCCTACACCTGTTGACACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGA 2640
Qy 2891 GACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2950
Db 2641 GACAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2700
Qy 2951 ATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 3010
Db 2701 ATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 2760
Qy 3011 CGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAGACT 3070
Db 2761 CGTCTCCCGCCCGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAAGACA 2820
Qy 3071 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 3130
Db 2821 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 2880
Qy 3131 CGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 3190
Db 2881 CGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 2940
Qy 3191 AGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 3250
Db 2941 GGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAGAACACC 3000
Qy 3251 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGAC 3310
Db 3001 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGAC 3060
Qy 3311 TCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3370

```
Db       3061 TCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3120
Qy       3371 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3430
Db       3121 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3180
Qy       3431 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3490
Db       3181 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3240
Qy       3491 CAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3550
Db       3241 CAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3300
Qy       3551 TACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3610
Db       3301 TACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3360
Qy       3611 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGATGGTTACAAT 3670
Db       3361 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGTTACAAT 3420
Qy       3671 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3730
Db       3421 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3480
Qy       3731 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAG 3790
Db       3481 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAG 3540
Qy       3791 TTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3850
Db       3541 TTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3600
Qy       3851 GTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTG 3910
Db       3601 GTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTG 3660
Qy       3911 AACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTC 3970
Db       3661 AACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTC 3720
Qy       3971 AATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACG 4030
Db       3721 AATATGGAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACG 3780
Qy       4031 GATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 4090
Db       3781 GATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 3840
Qy       4091 CCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTC 4150
Db       3841 CCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTC 3900
Qy       4151 TTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 4210
Db       3901 TTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 3960
Qy       4211 AGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGCAGTTGAAGCT 4270
Db       3961 AGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTTGAAGCT 4020
Qy       4271 CAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATTAAA 4330
Db       4021 CAGATGCCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATTAAA 4080
Qy       4331 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4390
Db       4081 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4140
Qy       4391 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4450
Db       4141 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4200
Qy       4451 TTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4510
Db       4201 TTGCAACCAGGTCAAGTCAATGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4260
Qy       4511 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4570
Db       4261 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4320
Qy       4571 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAAATCCCGTAAA 4630
Db       4321 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCCAAATCCCGTAAA 4380
Qy       4631 TCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGGTGCTCGAAGG 4690
Db       4381 TCCAAAACTCCAGATCCCTTCAGCGATACCGAGGTATCACCAGAACGTGGTGCTCGAAGG 4440
Qy       4691 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4750
Db       4441 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4500
Qy       4751 CCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGCTCAGATGGCG 4810
Db       4501 CCTAGCAGGACCAACTTGTATGGGAGCCAAGTTGGTTTAAACTCAAACGCTCAGATGGCG 4560
Qy       4811 ACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAA 4870
Db       4561 ACGCCCACGCAAGACAGGAAGCAGATGACGACGAGCACTCTCGCGCAGTCGGCTACGGAA 4620
Qy       4871 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTAT 4930
Db       4621 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGCTTGAAGCTCATCAATGAGTACTTTTAT 4680
Qy       4931 GGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTGGGTGACCACC 4990
Db       4681 GGAGTCAGGATCTACCCAGGTCAGGACCCAACACACGTGTACATCGGCTGGGTGACCACC 4740
Qy       4991 CAGTACCACT 5000
Db       4741 CAGTACCACT 4750
```

RESULT 3
US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:

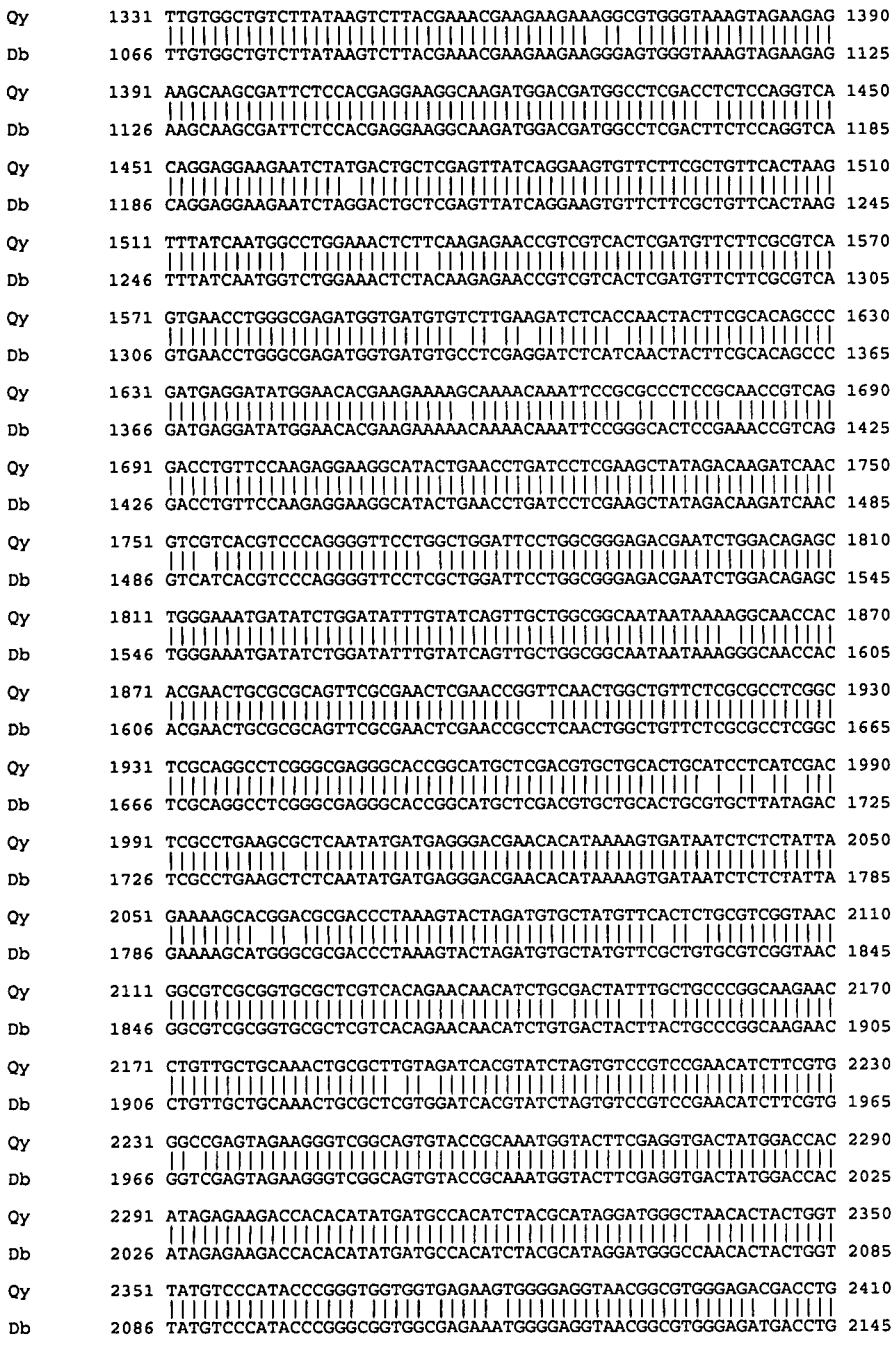
```
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv2
US-10-668-767-129

  Query Match             90.0%;  Score 4501.6;  DB 8;  Length 15405;
  Best Local Similarity   97.1%;  Pred. No. 0;
  Matches 4614;  Conservative    0;  Mismatches  109;  Indels   27;  Gaps    2;

Qy        251 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAA 310
Db          1 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCATTCTTGCGTACGGAA 60

Qy        311 GACATGGTGTGCATGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 370
Db         61 GACATGGTGTGCCTGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 120

Qy        371 CTCGGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTG 430
Db        121 TTCGGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCACCTGATCTG 180

Qy        431 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490
Db        181 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 240

Qy        491 ACAGCTGCGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTAT 550
Db        241 ACGGCTGCGGGTTCTGAAACT---------------GGTAAAGGTACCGGTTCTGGTCAT 285

Qy        551 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 610
Db        286 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 345

Qy        611 GCCTGCCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 670
Db        346 GCCTGCCTGTCGACATCATCATCCCAGGATAAGCCGGCCTTTGACGTGGGTCTGCAACAG 405

Qy        671 CACTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 730
Db        406 CACTCCCAGGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 465

Qy        731 GGCGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATAC 790
Db        466 GGTGAGAAGGTGCGAGTCGGAGATGACTTGATTCTGGTCTCCGTGGCTACTGAGAGATAC 525

Qy        791 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCAC 850
Db        526 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACCCAC 585

Qy        851 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTC 910
Db        586 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTAGGCTATGTGTTC 645

Qy        911 GGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACT 970
Db        646 GGAGGTGATGTGCTGCGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGTACC 705

Qy        971 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAA 1030
Db        706 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACGAAGGAGGTTCAGTGATGTCTCAA 765

Qy       1031 GCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 1090
Db        766 GCCCGGTCTTTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 825

Qy       1091 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGAC 1150
Db        826 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTCGGAGTAAACGAC 885

Qy       1151 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGC 1210
Db        886 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAAGCCACAACAGCTTCCTGTGCCTTCTGC 945

Qy       1211 CTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1270
Db        946 CTGCGTCAGGAGAAGGATGATCAGAAACAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1005

Qy       1271 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGC 1330
Db       1006 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACTGGC 1065

Qy       1331 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAG 1390
Db       1066 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGGAGGGAGTGGGTAAAGTAGAAGAG 1125

Qy       1391 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCA 1450
Db       1126 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGACGGCCTCGACTTCTCCAGGTCA 1185

Qy       1451 CAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAG 1510
Db       1186 CAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGAAAGTGTTCTTCGCTGTTCACTAAG 1245

Qy       1511 TTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1570
Db       1246 TTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1305

Qy       1571 GTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCC 1630
Db       1306 GTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAACCC 1365

Qy       1631 GATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAG 1690
Db       1366 GATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAG 1425

Qy       1691 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAC 1750
Db       1426 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAC 1485

Qy       1751 GTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGC 1810
Db       1486 GTCATCACGTCTCAGGGGTTCCTGGCTGGTTTCCTGGCGGGAGACGAATCTGGACAGAGC 1545

Qy       1811 TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCAC 1870
Db       1546 TGGGAAATGATATCTGGATATTTGTATCAGTTGTTGGCGGCAATAATAAAGGGCAACCAC 1605

Qy       1871 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGC 1930
Db       1606 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTGAACTGGCTGTTCTCGCGCCTCGGC 1665

Qy       1931 TCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGAC 1990
Db       1666 TCGCAGGCCTCGGGCGAGGGCACTGGCATGCTCGACGTGCTGCACTGCGTGCTCATCGAC 1725

Qy       1991 TCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 2050
Db       1726 TCGCCTGAAGCGTTGAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 1785

Qy       2051 GAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAAC 2110
Db       1786 GAAAAGCACGGGCGCGACCCTAAAGTACTAGATGTGTTATGTTCACTCTGCGTCGGTAAC 1845

Qy       2111 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAAC 2170
Db       1846 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTATTTGCTGCCCGGCAAGAAC 1905

Qy       2171 CTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 2230
Db       1906 CTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 1965

Qy       2231 GGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCAC 2290
Db       1966 GGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAAGTGACTATGGACCAC 2025

Qy       2291 ATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGCTAACACTACTGGT 2350
```

```
Db       2026 ATAGAGAAGACCACACATATGATACCACATCTACGCATAGGATGGGCTAACACTACTGGC 2085
Qy       2351 TATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTG 2410
Db       2086 TACGTCCCATACCCGGGTGGTGGTGAAAAGTGGGGAGGTAACGGCGTGGGAGACGACCTG 2145
Qy       2411 TACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAAT 2470
Db       2146 TACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAAACTCCCGTCAAT 2205
Qy       2471 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGAC 2530
Db       2206 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCGTTAGAC 2265
Qy       2531 CTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2590
Db       2266 CTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2325
Qy       2591 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGT 2650
Db       2326 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAATTGAGTTGC 2385
Qy       2651 CGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCC 2710
Db       2386 CGGTTCCTGCTGGGCGGGGAACATGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCC 2445
Qy       2711 CCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTC 2770
Db       2446 CCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCTTGCTTCTACTTC 2505
Qy       2771 GGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTT 2830
Db       2506 GGCAACCTGTCCAAGCGCGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTT 2565
Qy       2831 GTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGA 2890
Db       2566 GTGCCTACACCTGTTGACACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGA 2625
Qy       2891 GACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2950
Db       2626 GACAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2685
Qy       2951 ATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 3010
Db       2686 ATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 2745
Qy       3011 CGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAGACT 3070
Db       2746 CGTCTCCCGCCCGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAAGACA 2805
Qy       3071 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 3130
Db       2806 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 2865
Qy       3131 CGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 3190
Db       2866 CGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 2925
Qy       3191 AGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 3250
Db       2926 AGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAGAACACC 2985
Qy       3251 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGAC 3310
Db       2986 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGAC 3045
Qy       3311 TCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3370
Db       3046 TCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3105
Qy       3371 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3430
Db       3106 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3165

Qy       3431 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3490
Db       3166 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3225
Qy       3491 CAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3550
Db       3226 CAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3285
Qy       3551 TACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3610
Db       3286 TACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3345
Qy       3611 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGATGGTTACAAT 3670
Db       3346 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGTTACAAT 3405
Qy       3671 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3730
Db       3406 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3465
Qy       3731 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAG 3790
Db       3466 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAG 3525
Qy       3791 TTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3850
Db       3526 TTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3585
Qy       3851 GTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTG 3910
Db       3586 GTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTA 3645
Qy       3911 AACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTC 3970
Db       3646 AACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTC 3705
Qy       3971 AATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACG 4030
Db       3706 AATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACG 3765
Qy       4031 GATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 4090
Db       3766 GATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 3825
Qy       4091 CCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTC 4150
Db       3826 CCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTC 3885
Qy       4151 TTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 4210
Db       3886 TTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 3945
Qy       4211 AGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGCAGTTGAAGCT 4270
Db       3946 AGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTTGAAGCT 4005
Qy       4271 CAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATTAAA 4330
Db       4006 CAGATGCCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATTAAA 4065
Qy       4331 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4390
Db       4066 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4125
Qy       4391 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4450
Db       4126 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4185
Qy       4451 TTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4510
Db       4186 TTGCAACCAGGTCAAGTCAATGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4245
```

```
Qy       4511 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4246 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4305

Qy       4571 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAAATCCCGTAAA 4630
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       4306 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCCAAATCCCGTAAA 4365

Qy       4631 TCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGGTGCTCGAAGG 4690
             |||||||| ||||| |||||||| |||||||| ||||||||||||||||||||||||||||
Db       4366 TCCAAAACTCCAGATCCCTTCAGCGATACCGAGGTATCACCAGAACGTGGTGCTCGAAGG 4425

Qy       4691 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4750
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4426 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4485

Qy       4751 CCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGCTCAGATGGCG 4810
             ||||||||||||||| |||||||||||||||||||| |||              ||||||
Db       4486 CCTAGCAGGACCAACTTGTATGGGAGCCAAGTTGGTTTAAAC------------ATGGCG 4533

Qy       4811 ACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAA 4870
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       4534 ACGCCCACGCAAGACAGGAAGCAGATGACGACGAGCACTCTCGCGCAGTCGGCTACGGAA 4593

Qy       4871 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTAT 4930
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4594 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGCTTGAAGCTCATCAATGAGTACTTTTAT 4653

Qy       4931 GGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTGGGTGACCACC 4990
             |||||||||||||||||||||| |||||||| ||| |||||||||||||||||||||||||
Db       4654 GGAGTCAGGATCTACCCAGGTCAGGACCCAACACACGTGTACATCGGCTGGGTGACCACC 4713

Qy       4991 CAGTACCACT 5000
             ||||||||||
Db       4714 CAGTACCACT 4723
```

```
RESULT 4
US-10-668-767-127
; Sequence 127, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
;   LENGTH: 15387
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15384)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv7
US-10-668-767-127

  Query Match             89.5%;  Score 4472.8;  DB 8;  Length 15387;
  Best Local Similarity   96.8%;  Pred. No. 0;
```

```
  Matches 4596;  Conservative    0;  Mismatches  127;  Indels   27;  Gaps    2;

Qy        251 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAA 310
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCATTCTTGCGTACGGAA 60

Qy        311 GACATGGTGTGCATGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 370
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATGGTGTGCCTGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGT 120

Qy        371 CTCGGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTG 430
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 TTCGGCAACCGGCACTGCTTCTTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTG 180

Qy        431 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 TCGCAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAAGAGTTGGTA 240

Qy        491 ACAGCTGCGGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTAT 550
              |||||||||| |||||||||                ||||||||||||||||||||| ||
Db        241 ACAGCTGCGGGCTCTGAAACT--------------GGTAAAGGTACCGGTTCTGGTCAT 285

Qy        551 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 610
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTG 345

Qy        611 GCCTGCCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 670
              |||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db        346 GCCTGCCTGTCGACATCATCCTCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 405

Qy        671 CACTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 730
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 CACTCCCAGGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAG 465

Qy        731 GGCGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATAC 790
              || |||||||||||||||||||||||||||||||| |||||||||| | ||||||||||
Db        466 GGTGAGAAGGTGCGAGTCGGAGATGACTTGATTCTGGTCTCCGTGGCTACTGAGAGATAC 525

Qy        791 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCAC 850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 TTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCAC 585

Qy        851 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTC 910
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||| |||
Db        586 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTAGGCTATGTATTC 645

Qy        911 GGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACT 970
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GGAGGTGATGTGCTGCGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACC 705

Qy        971 TGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAA 1030
              |||||||||||||||||||||||||||||| ||| |||||||||| ||||||||||||
Db        706 TGGACAAAGGATGGGGGGCAAAATATCGTAGTGTACGAAGGAGGTTCGGTGATGTCTCAA 765

Qy       1031 GCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 1090
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 GCCCGTTCTCTATGGCGCCTGGAACTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAAC 825

Qy       1091 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGAC 1150
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||
Db        826 TGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTCGGAGTAAACGAC 885

Qy       1151 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGC 1210
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        886 CAGAATGAGCTGTATTTAGTTAGCAGAGAGGAAGCCACAACAGCTTCCTGTGCCTTCTGC 945

Qy       1211 CTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1270
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 CTGCGTCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATA 1005

Qy       1271 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGC 1330
              |||||||||||||||| || |||||||||||||||||||||||||||| |||||||||
Db       1006 GGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACTGGC 1065
```

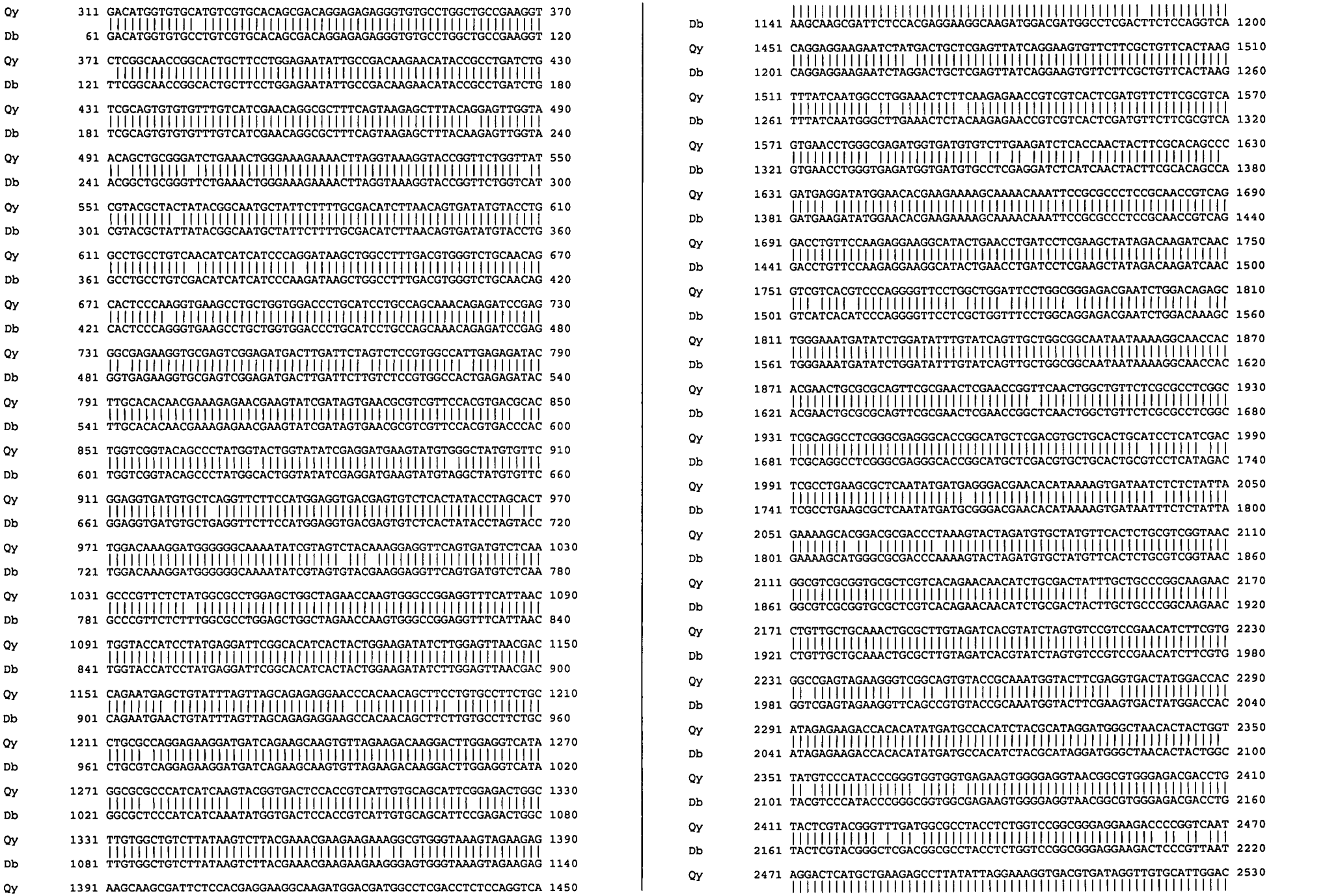

Qy 1331 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAG 1390
Db 1066 TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAAGAG 1125
Qy 1391 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCA 1450
Db 1126 AAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGGTCA 1185
Qy 1451 CAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAG 1510
Db 1186 CAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAG 1245
Qy 1511 TTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1570
Db 1246 TTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCA 1305
Qy 1571 GTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCC 1630
Db 1306 GTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAGCCC 1365
Qy 1631 GATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAG 1690
Db 1366 GATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCGTCAG 1425
Qy 1691 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAC 1750
Db 1426 GACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAC 1485
Qy 1751 GTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGC 1810
Db 1486 GTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGC 1545
Qy 1811 TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCAC 1870
Db 1546 TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAACCAC 1605
Qy 1871 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGC 1930
Db 1606 ACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCTCGGC 1665
Qy 1931 TCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGAC 1990
Db 1666 TCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTTATAGAC 1725
Qy 1991 TCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 2050
Db 1726 TCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTA 1785
Qy 2051 GAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAAC 2110
Db 1786 GAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAAC 1845
Qy 2111 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAAC 2170
Db 1846 GGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGCAAGAAC 1905
Qy 2171 CTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 2230
Db 1906 CTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTG 1965
Qy 2231 GGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCAC 2290
Db 1966 GGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCAC 2025
Qy 2291 ATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGT 2350
Db 2026 ATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACTACTGGT 2085
Qy 2351 TATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTG 2410
Db 2086 TATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGACCTG 2145
Qy 2411 TACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAAT 2470
Db 2146 TACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCCGTCAAT 2205
Qy 2471 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGAC 2530
Db 2206 AGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGAC 2265
Qy 2531 CTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2590
Db 2266 CTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACC 2325
Qy 2591 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGT 2650
Db 2326 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGT 2385
Qy 2651 CGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCC 2710
Db 2386 CGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGCTACTCT 2445
Qy 2711 CCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTC 2770
Db 2446 CCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTC 2505
Qy 2771 GGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTT 2830
Db 2506 GGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACGGCCTTC 2565
Qy 2831 GTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGA 2890
Db 2566 GTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATTAGA 2625
Qy 2891 GACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2950
Db 2626 GATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG 2685
Qy 2951 ATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 3010
Db 2686 ATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAG 2745
Qy 3011 CGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAGACT 3070
Db 2746 CGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAAGACT 2805
Qy 3071 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 3130
Db 2806 ATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTT 2865
Qy 3131 CGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 3190
Db 2866 CGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTG 2925
Qy 3191 AGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 3250
Db 2926 AGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAGAACACC 2985
Qy 3251 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGAC 3310
Db 2986 CACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAATGAGGAC 3045
Qy 3311 TCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3370
Db 3046 TCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAG 3105
Qy 3371 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3430
Db 3106 AAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATG 3165
Qy 3431 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3490
Db 3166 CTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAG 3225
Qy 3491 CAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3550

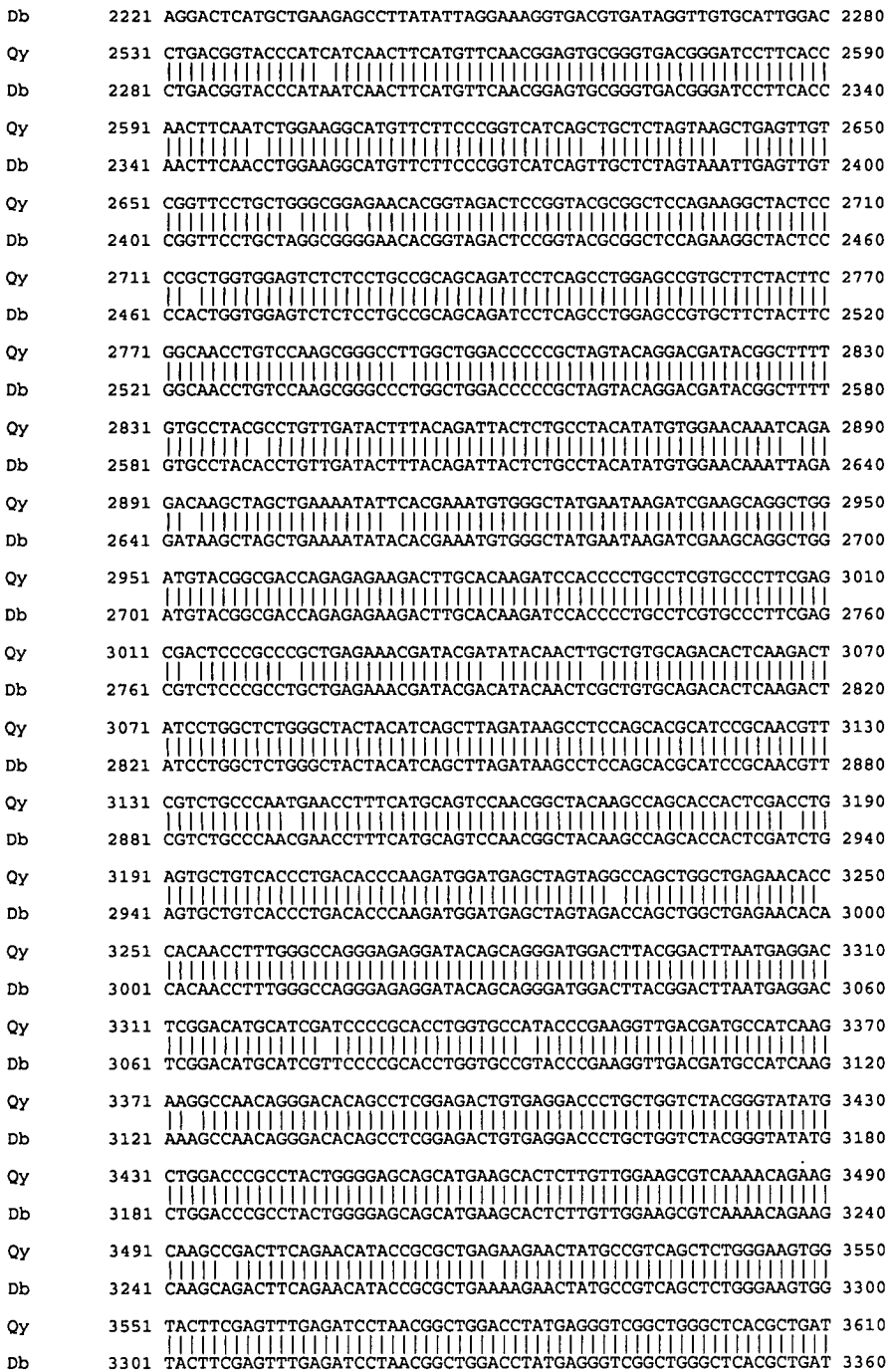
```
Db       3226 CAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGG 3285

Qy       3551 TACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3610

Db       3286 TACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGAT 3345

Qy       3611 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGATGGTTACAAT 3670

Db       3346 ATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAAT 3405

Qy       3671 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3730

Db       3406 GAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGAC 3465

Qy       3731 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAG 3790

Db       3466 GTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAATGGTGAG 3525

Qy       3791 TTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3850

Db       3526 TTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAACTTT 3585

Qy       3851 GTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTG 3910

Db       3586 GTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAAGATGTG 3645

Qy       3911 AACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTC 3970

Db       3646 AATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTTTGCGTC 3705

Qy       3971 AATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACG 4030

Db       3706 AATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAGAATACT 3765

Qy       4031 GATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 4090

Db       3766 GATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGATACACCT 3825

Qy       4091 CCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTC 4150

Db       3826 CCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGGGAGTTC 3885

Qy       4151 TTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 4210

Db       3886 TTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCC 3945

Qy       4211 AGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGCAGTTGAAGCT 4270

Db       3946 AGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTTGAAGCT 4005

Qy       4271 CAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATTAAA 4330

Db       4006 CAGATGCCCGCCCATATTGACCAGATCATGAGGAGCGGTTTCACCATGAACGATATCAAA 4065

Qy       4331 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4390

Db       4066 GGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCT 4125

Qy       4391 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4450

Db       4126 TCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGTTACTATACAAAATTACAATAAT 4185

Qy       4451 TTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4510

Db       4186 TTGCAACCAGGCCAAGTCAACGGCATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAG 4245

Qy       4511 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4570

Db       4246 TATGACTTGGGAGCGCAAGGTTTGACGCCTGATGATAAGAAGGACAAGAGGGGACGATCG 4305

Qy       4571 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAAATCCCGTAAA 4630

Db       4306 CCTTTCAAGTTCTTCAGAAGCAAGCGCGGCGAAAGCAGTGATCGTGCTAAATCCCGTAAA 4365

Qy       4631 TCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGGTGCTCGAAGG 4690

Db       4366 TCCAAAACACCAGACCCCTTCAGTGATACCGAAGTATCACCAGAACGTGGTGCTCGAAGG 4425

Qy       4691 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4750

Db       4426 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4485

Qy       4751 CCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGCTCAGATGGCG 4810

Db       4486 CCTAGCAGGACCAACTTGTATGGGAGCCAAGTTGGTTTGAAC----------ATGGCG 4533

Qy       4811 ACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAA 4870

Db       4534 ACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAA 4593

Qy       4871 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTAT 4930

Db       4594 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTAT 4653

Qy       4931 GGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTGGGTGACCACC 4990

Db       4654 GGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACGTGTACATCGGCTGGGTGACCACC 4713

Qy       4991 CAGTACCACT 5000

Db       4714 CAGTACCACT 4723
```

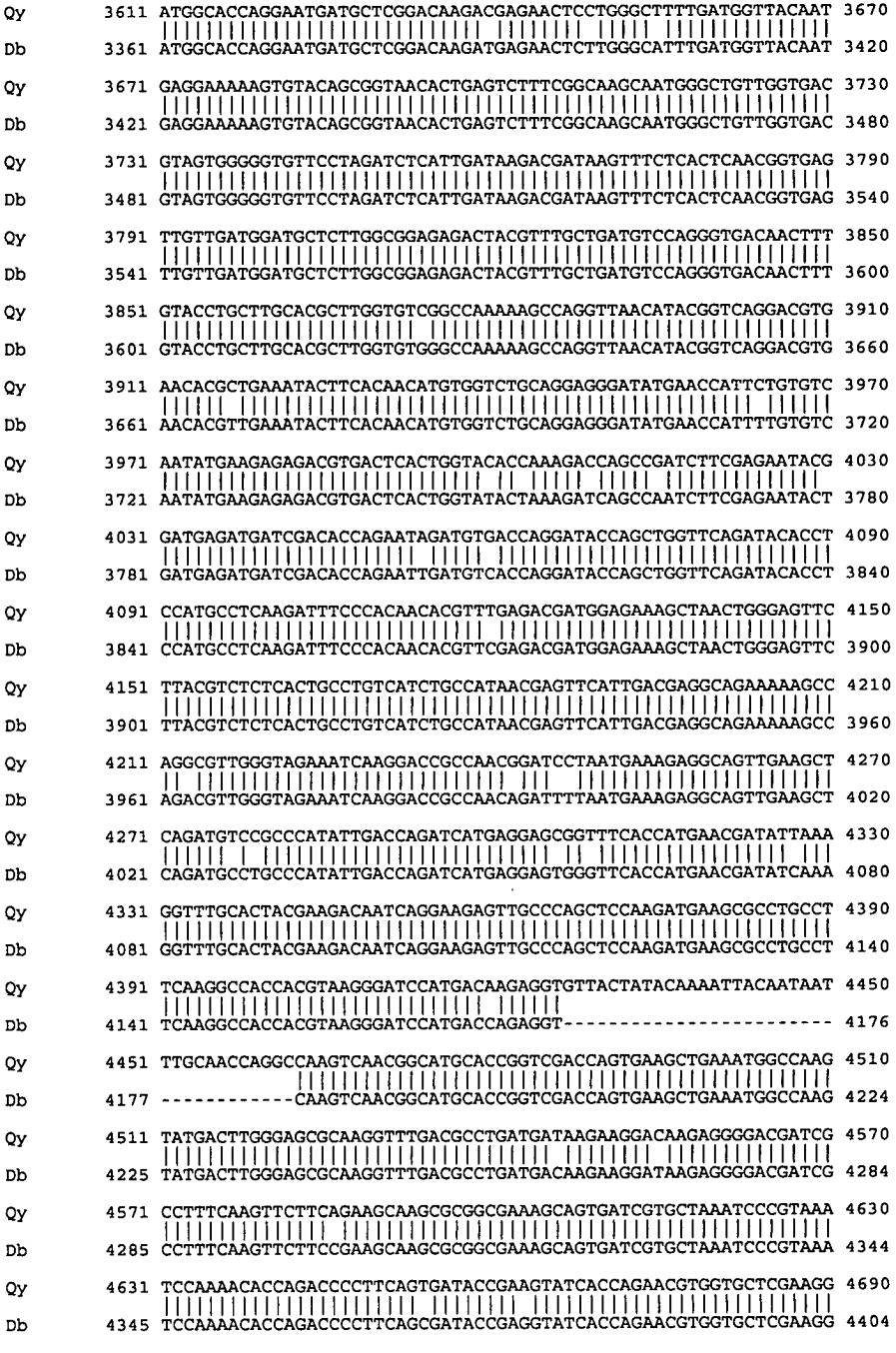
RESULT 5
US-10-668-767-145
; Sequence 145, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 15303
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15300)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv6
US-10-668-767-145

Query Match 85.8%; Score 4288.8; DB 8; Length 15303;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 4502; Conservative 0; Mismatches 137; Indels 111; Gaps 2;

```
Qy        251 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAA 310

Db          1 ATGGCGGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCATTCTTGCGTACGGAA 60
```





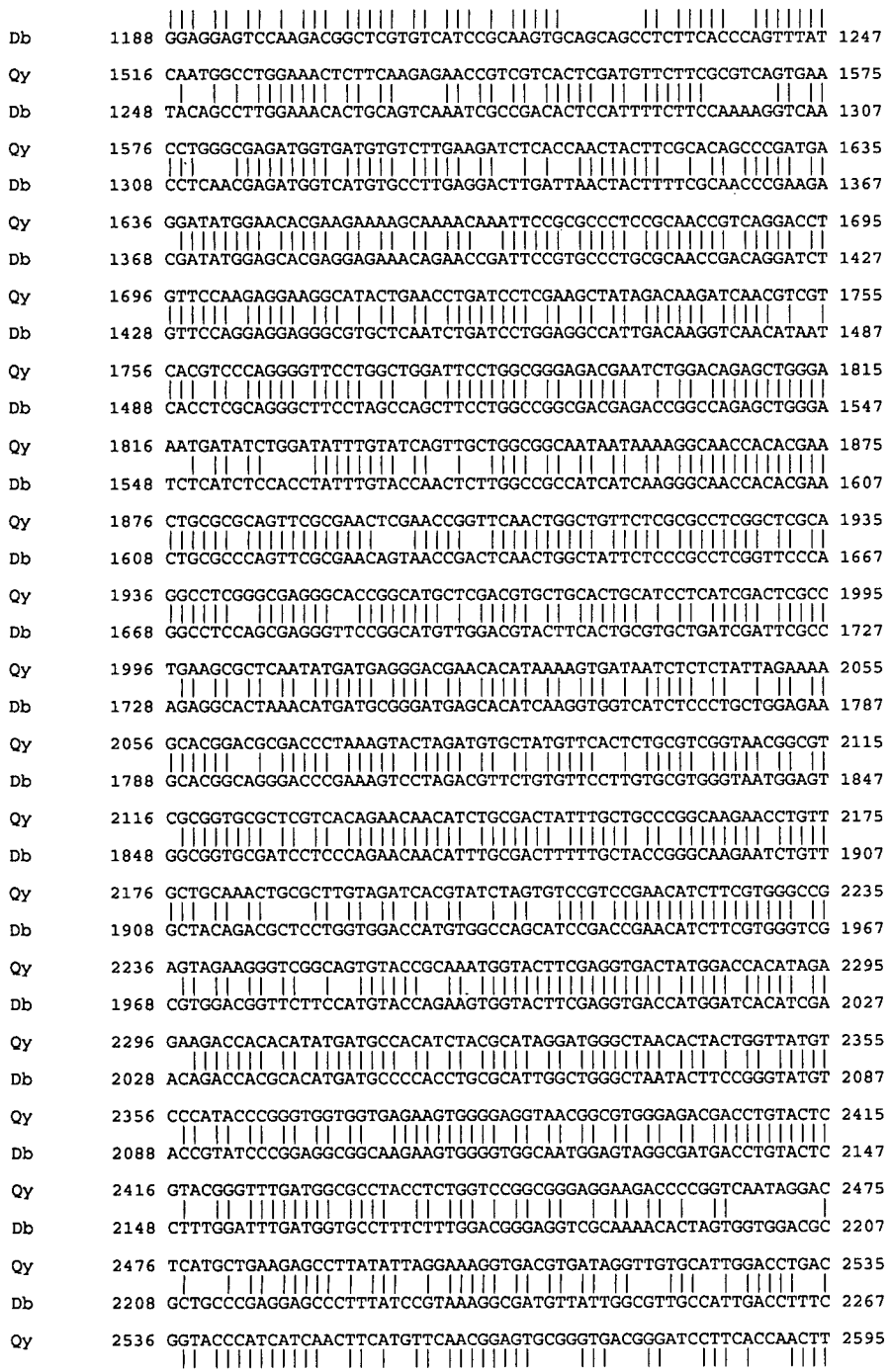


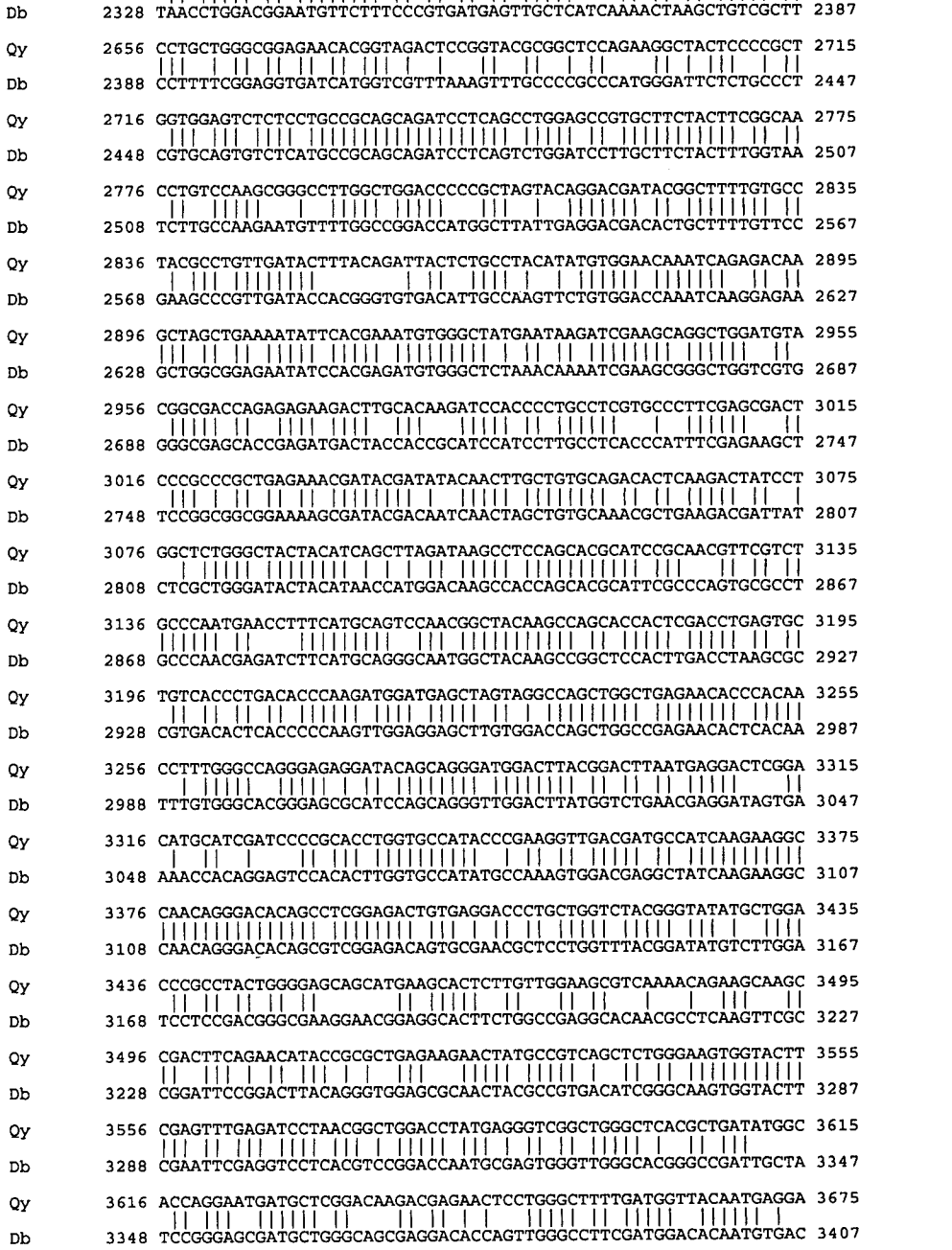
```
Qy       4691 CCTAACCCTCAGATCAAAGTGTCACAGGCCAATCAAAGATATAACGGCATGAACGCGCGT 4750
              || ||||||||||||||||||||||||
Db       4405 CCCAACCCTCAGATCAAAGTGTCACAG------------------------------- 4431

Qy       4751 CCTAGCAGGACCAACCTGTATGGGAGCCAAGTTGGTTTGAACTCGAACGCTCAGATGGCG 4810
                                                    ||||||||||||||||||
Db       4432 -----------------------------------------TCGAACGCTCAGATGGCG 4449

Qy       4811 ACGCCCACGCAAGACAGGAAGCAGATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAA 4870
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       4450 ACGCCCACGCAAGACAGGAAGCAGATGACGACGAGCACTCTCGCGCAGTCGGCTACGGAA 4509

Qy       4871 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTAT 4930
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       4510 ACTGTCGGCAATGAGATCTTCGATGCAGAGTGCTTGAAGCTCATCAATGAGTACTTTTAT 4569

Qy       4931 GGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTACATCGGCTGGGTGACCACC 4990
              |||||||||||||||||||||||| |||||||| ||| |||||||||| ||||||||||
Db       4570 GGAGTCAGGATCTACCCAGGTCAGGACCCAACACACGTGTACATCGGTTGGGTGACCACC 4629

Qy       4991 CAGTACCACT 5000
              ||||||||||
Db       4630 CAGTACCACT 4639
```

RESULT 6
US-10-668-767-9
; Sequence 9, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16363
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15890)..(15890)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15327)
; OTHER INFORMATION:
US-10-668-767-9

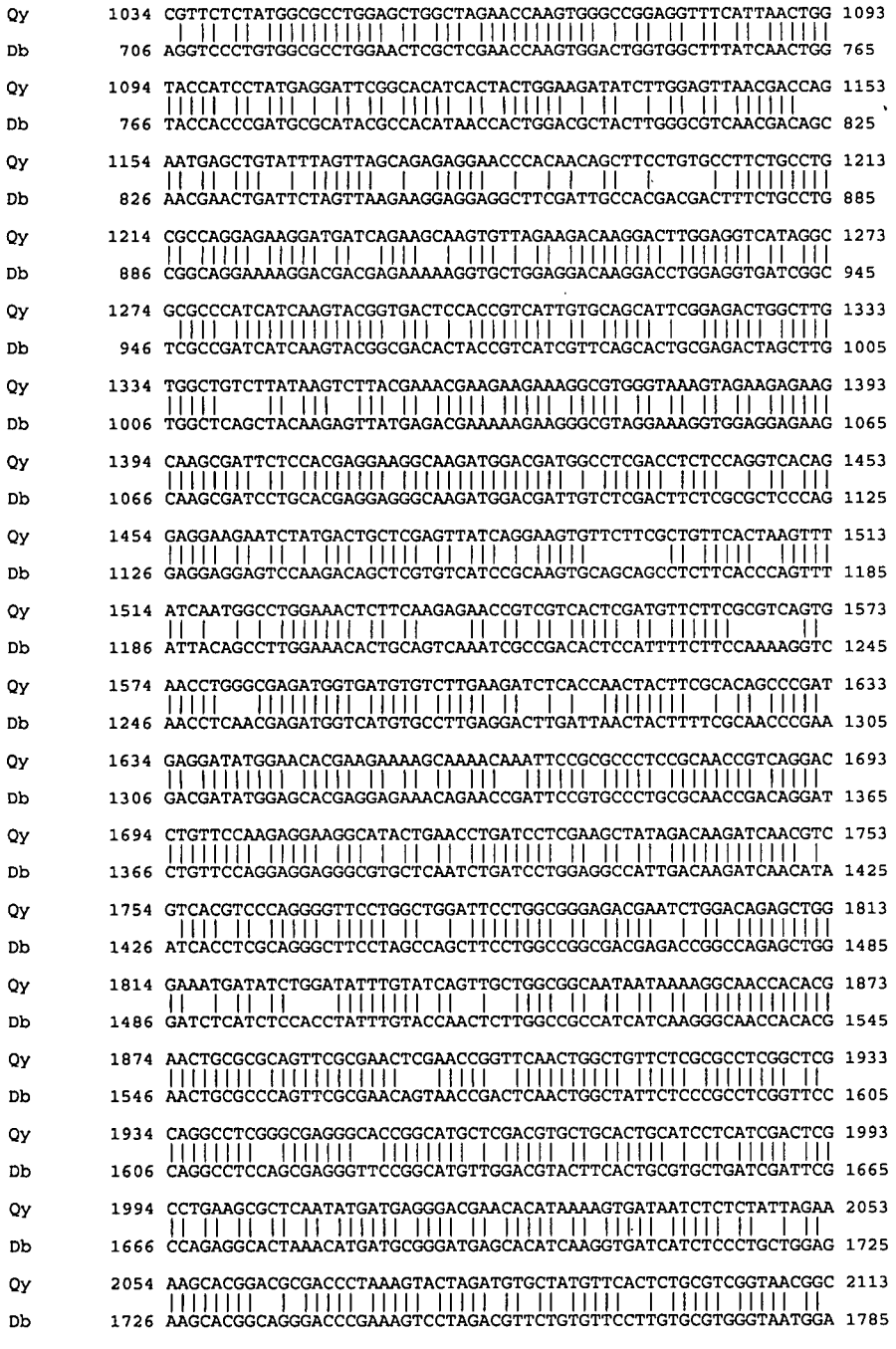
Query Match 43.7%; Score 2185.8; DB 8; Length 16363;
Best Local Similarity 70.7%; Pred. No. 0;
Matches 2983; Conservative 0; Mismatches 1192; Indels 42; Gaps 4;

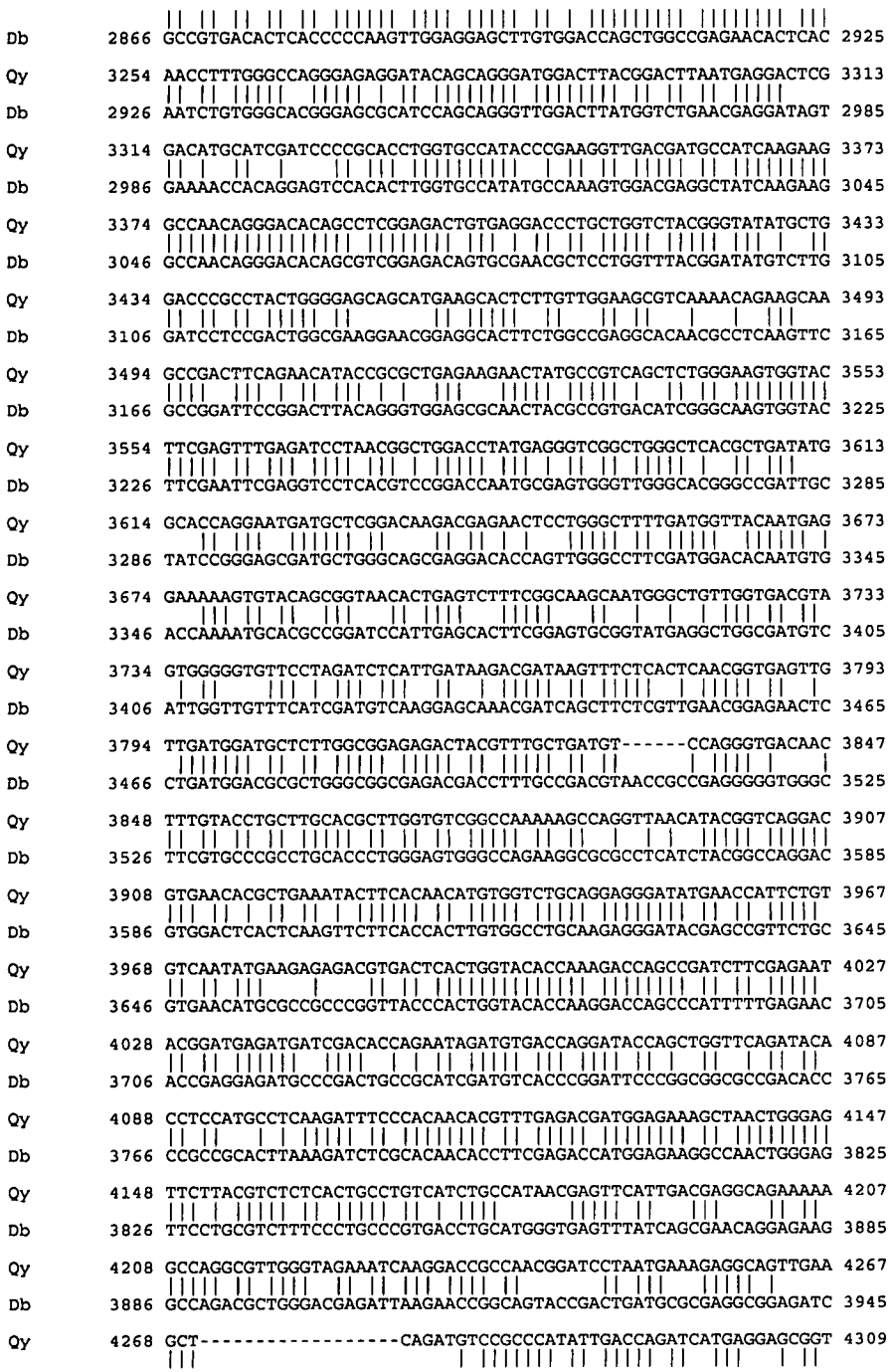
```
Qy        256 GGAAGCAGAGGGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAAGACAT 315
              ||  |  | || |||||    |||||| |||||||||||| || || | ||||| |||||
Db          3 GGCTGAGGCGGAGGGAGGCTCCGAGCAGGATGATGTTTCATTCCTGAGAACGGAGGACAT 62

Qy        316 GGTGTGCATGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGG 375
              |||     | || ||||| ||||| || ||| | || ||| |||| ||||||||  | ||
Db         63 GGTCACGCTCTCCTGCACGGCGACGGGGGAGCGTGTCTGCTTGGCCGCCGAAGGATTTGG 122

Qy        376 CAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTGTCGCA 435
              |||||||||||||||| || ||||||||||||||||||| | ||||| ||||| |||||
Db        123 CAACCGGCACTGCTTTCTCGAGAATATTGCCGACAAGAACGTGCCGCCGGATCTTTCGCA 182

Qy        436 GTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGC 495
              |||||| || |||||||| |||||||| || ||  |||| || |||||||||||| || ||
Db        183 GTGTGTCTTCGTCATCGAGCAGGCGCTGTCCGTGCGAGCATTGCAGGAGTTGGTGACGGC 242

Qy        496 TGCGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTAC 555
              || ||||| || |||                || ||||| ||||| || ||  |  | ||
Db        243 GGCAGGATCCGAGACT--------------GGCAAAGGCACCGGATCGGGACACAGGAC 287

Qy        556 GCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTG 615
              | ||| || |||||||| ||| |  |||| || |  ||||||||||||||| |||| ||
Db        288 ATTGCTCTATGGCAATGCCATTTTGCTGCGTCACCACAACAGTGATATGTACTTGGCATG 347

Qy        616 CCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCACTC 675
              ||||| || || || ||  | || |||||| |||| |||||||| |||||  |||||
Db        348 TCTGTCCACCTCCTCGTCGAACGACAAGCTGTCCTTCGACGTGGGCCTGCAGGAGCACAG 407

Qy        676 CCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCGA 735
              ||| || || || || |||||||| | ||||| || ||||| ||| | || ||||||||
Db        408 CCAGGGAGAGGCTTGTTGGTGGACGGTTCATCCGGCGAGCAAGCAGCGCTCTGAGGGCGA 467

Qy        736 GAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTGCA 795
              |||||||| |||||||||    |||| |  || ||||||||  ||  | || |||||
Db        468 GAAGGTGCGCGTCGGAGATGGTCTGATCCCGGTGTCCGTGGCCACCGAACGTTATTTGCA 527

Qy        796 CACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCACTGGTC 855
              || || || |||||||||  || || || || ||    ||||| ||||| ||||||||
Db        528 TACGACCAAGGAGAACGAACAGTCTATTGTAAATGCCAGCTTCCATGTGACCCACTGGTC 587

Qy        856 GGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTCGGAGG 915
              || |||||||| || || || || || |||||||||||  |||||||||||  || || ||
Db        588 CGTGCAGCCCTACGGCACGGGCATCTCTAGGATGAAGTACGTGGGCTATGTCTTTGGCGG 647

Qy        916 TGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACTTGGAC 975
              |||||||| | |||||||||| || |||||||| || || ||||| || || |||
Db        648 CGATGTGCTGCGTTTCTTCCATGGTGGCGACGAGTGCCTGACCATACCGAGTACATGGGG 707

Qy        976 AAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCCCG 1035
                || | ||| |||||||| ||  | ||| | || ||    || ||| | || ||  |
Db        708 TCGTGAGGCGGGACAAAATATTGTTATTTACGAGGGCGGCGTGGTCATGGCACAGGCGAG 767

Qy       1036 TTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAACTGGTA 1095
              || || |||||||||| || ||| |||||||||||||| || || || || ||||||||
Db        768 GTCCCTGTGGCGCCTGGAACTCGCTCGAACCAAGTGGGCTGGTGGCTTTATCAACTGGTA 827

Qy       1096 CCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGACCAGAA 1155
              ||| || ||| | || || ||||| || |||||| | ||  | || || |||||    ||
Db        828 CCACCCGATGCGCATACGCCACATAACCACTGGACGCTACTTGGGCGTCAACGACAGCAA 887

Qy       1156 TGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGCCTGCG 1215
              || |||  | ||||||  | |||||  |  | |  ||  |     | ||||||||||||
Db        888 CGAACTGATTCTAGTTAAGAAGGAGGAGGCTTCGATTGCCACGACGACTTTCTGCCTGCG 947

Qy       1216 CCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATAGGCGC 1275
              ||||| ||||| ||  ||||  | ||| | || |||||||||| ||||||| || ||| |
Db        948 GCAGGAAAAGGACGACGAGAAAAAGGTGCTGGAGGACAAGGACCTGGAGGTGATCGGCTC 1007

Qy       1276 GCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTGTG 1335
              ||| |||||||||||||| ||| | |||||||| || ||||| |  |||||| |||||||
Db        1008 GCCGATCATCAAGTACGGCGACACTACCGTCATCGTCCAGCACTGCGAGACTAGCTTGTG 1067

Qy       1336 GCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCA 1395
              |||    || |||  ||| || ||||| ||||| ||||| || || || || ||||||||
Db        1068 GCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTGGAGGAGAAGCA 1127

Qy       1396 AGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGA 1455
              |||||| || |||||||| |||||||||||||||| | |||||| |||| | || |||||
Db        1128 AGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCGCGCTCCCAGGA 1187

Qy       1456 GGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTAT 1515
```

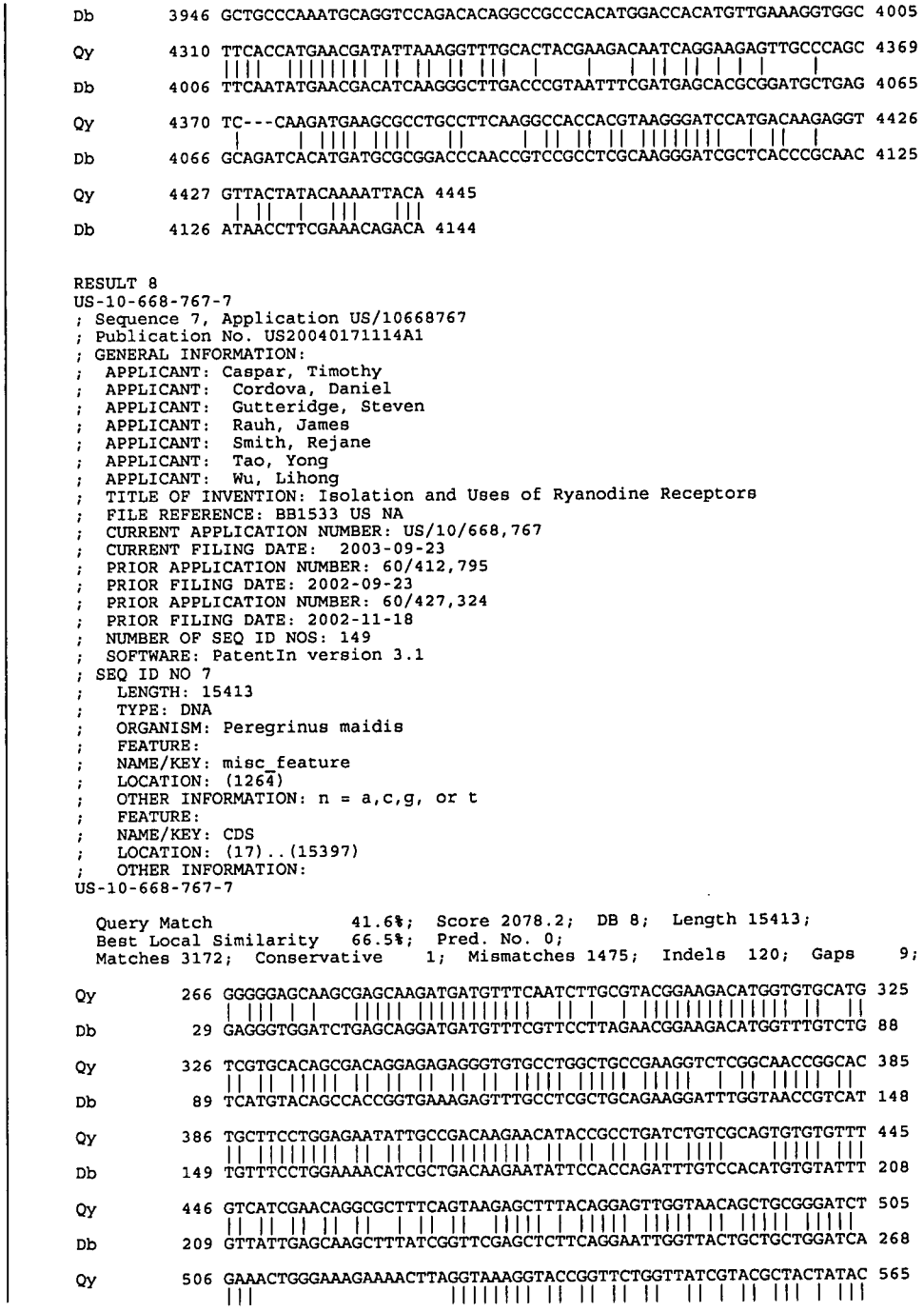




```
Qy       3676 AAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGACGTAGT 3735
Db       3408 CAAAATGCACGCCGGATCCATTGAGCACTTCGGAGTGCGGTATGAGGCTGGCGATGTCAT 3467

Qy       3736 GGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAGTTGTT 3795
Db       3468 TGGTTGTTTCATCGATGTCAAGGAGCAAACGATCAGCTTCTCGTTGAACGGAGAACTCCT 3527

Qy       3796 GATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGT------CCAGGGTGACAACTT 3849
Db       3528 GATGGACGCGCTGGGCGGCGAGACGACCTTTGCCGACGTAACCGCCGAGGGGGTGGGCTT 3587

Qy       3850 TGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGT 3909
Db       3588 CGTGCCCGCCTGCACCCTGGGAGTGGGCCAGAAGGCGCGCCTCATCTACGGCCAGGACGT 3647

Qy       3910 GAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGT 3969
Db       3648 GGACTCACTCAAGTTCTTCACCACTTGTGGCCTGCAAGAGGGATACGAGCCGTTCTGCGT 3707

Qy       3970 CAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATAC 4029
Db       3708 GAACATGCGCCGCCCGGTTACCCACTGGTACACCAAGGACCAGCCCATTTTTGAGAACAC 3767

Qy       4030 GGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACC 4089
Db       3768 CGAGGAGATGCCCGACTGCCGCATCGATGTCACCCGGATTCCCGGCGGCGCCGACACCCC 3827

Qy       4090 TCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTT 4149
Db       3828 GCCGCACTTAAAGATCTCGCACAACACCTTCGAGACCATGGAGAAGGCCAACTGGGAGTT 3887

Qy       4150 CTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAAAAAGC 4209
Db       3888 CCTGCGTCTTTCCCTGCCCGTGACCTGCATGGGTGAGTTTATCAGCGAACAGGAGAAGGC 3947

Qy       4210 CAGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGCAGTTGAAGC 4269
Db       3948 CAGACGCTGGGACGAGATTAAGAACCGGCAGTACCGACTAATGCGCGAGGCGGAGATCGC 4007

Qy       4270 T------------------CAGATGTCCGCCCATATTGACCAGATCATGAGGAGCGGTTT 4311
Db       4008 TGCCCAAATGCAGGTCCAGACACAGGCCGCCCACATGGACCACATGTTGAAAGGTGGCTT 4067

Qy       4312 CACCATGAACGATATTAAAGGTTTGCACTACGAAGACAATCAGGAAGAGTTGCCCAGCTC 4371
Db       4068 CAATATGAACGACATCAAGGGCTTGACCCGTAATTTCGATGAGCACGCGGATGCTGAGGC 4127

Qy       4372 ---CAAGATGAAGCGCCTGCCTTCAAGGCCACCACGTAAGGGATCCATGACAAGAGGTGT 4428
Db       4128 AGATCACATGATGCGCGGACCCAACCGTCCGCCTCGCAAGGGATCGCTCACCCGCAACAT 4187

Qy       4429 TACTATACAAAATTACA 4445
Db       4188 AACCTTCGAAACAGACA 4204


RESULT 7
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22562
;   LENGTH: 15606
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-22562

  Query Match             43.2%;  Score 2158.2;  DB 13;  Length 15606;
  Best Local Similarity   70.8%;  Pred. No. 0;
  Matches 2944;  Conservative    0;  Mismatches 1173;  Indels   42;  Gaps    4;

Qy        314 ATGGTGTGCATGTCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGTCTC 373
Db          1 ATGGTCACGCTCTCCTGCACGGCGACGGGGGAGCGTGTCTGCTTGGCCGCCGAAGGATTT 60

Qy        374 GGCAACCGGCACTGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTGTCG 433
Db         61 GGCAACCGGCACTGCTTTCTCGAGAATATTGCCGACAAGAACGTGCCGCCGGATCTTTCG 120

Qy        434 CAGTGTGTGTTTGTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACA 493
Db        121 CAGTGTGTCTTCGTCATCGAGCAGGCGCTGTCCGTGCGAGCATTGCAGGAGTTGGTGACG 180

Qy        494 GCTGCGGGATCTGAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGT 553
Db        181 GCGGCAGGATCCGAGACT--------------GGCAAAGGCACCGGATCGGGACACAGG 225

Qy        554 ACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCC 613
Db        226 ACATTGCTCTATGGCAATGCCATTTTGCTGCGTCACCACAACAGTGATATGTACTTGGCA 285

Qy        614 TGCCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCAC 673
Db        286 TGTCTGTCCACCTCCTCGTCGAACGACAAGCTGTCCTTCGACGTGGGCCTGCAGGAGCAC 345

Qy        674 TCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGC 733
Db        346 AGCCAGGGAGAGGCTTGTTGGTGGACGGTTCATCCGGCGAGCAAGCAGCGCTCTGAGGGC 405

Qy        734 GAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTG 793
Db        406 GAGAAGGTGCGCGTCGGAGATGATCTGATCCTGGTGTCCGTGGCCACCGAACGTTATTTG 465

Qy        794 CACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCACTGG 853
Db        466 CATACGACCAAGGAGAACGAACAGTCTATTGTAAATGCCAGCTTCCATGTGACCCACTGG 525

Qy        854 TCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTCGGA 913
Db        526 TCCGTGCAGCCCTACGGCACGGGCATCTCCAGGATGAAGTACGTGGGCTATGTCTTTGGC 585

Qy        914 GGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACTTGG 973
Db        586 GGCGATGTGCTGCGTTTCTTCCATGGTGGCGACGAGTGCCTGACCATACCGAGTACATGG 645

Qy        974 ACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCC 1033
Db        646 GGTCGTGAGGCGGGACAAAATATTGTTATTTACGAGGGCGGCGTGGTCATGGCACAGGCG 705
```

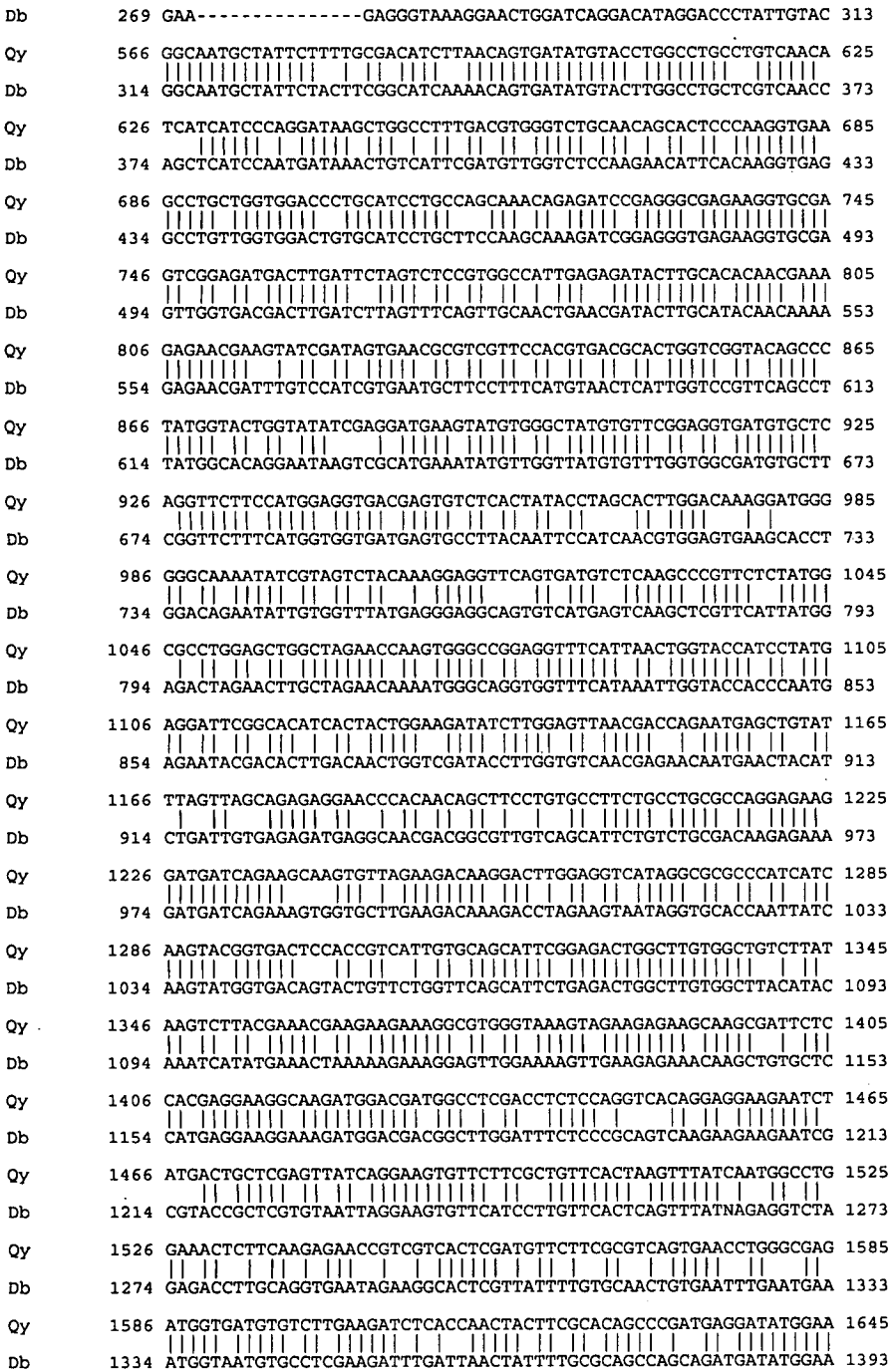

Qy 1034 CGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAACTGG 1093
Db 706 AGGTCCCTGTGGCGCCTGGAACTCGCTCGAACCAAGTGGACTGGTGGCTTTATCAACTGG 765
Qy 1094 TACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGACCAG 1153
Db 766 TACCACCCGATGCGCATACGCCACATAACCACTGGACGCTACTTGGGCGTCAACGACAGC 825
Qy 1154 AATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGCCTG 1213
Db 826 AACGAACTGATTCTAGTTAAGAAGGAGGAGGCTTCGATTGCCACGACGACTTTCTGCCTG 885
Qy 1214 CGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATAGGC 1273
Db 886 CGGCAGGAAAAGGACGACGAGAAAAAGGTGCTGGAGGACAAGGACCTGGAGGTGATCGGC 945
Qy 1274 GCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTG 1333
Db 946 TCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGCGAGACTAGCTTG 1005
Qy 1334 TGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAG 1393
Db 1006 TGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTGGAGGAGAAG 1065
Qy 1394 CAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAG 1453
Db 1066 CAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCGCGCTCCCAG 1125
Qy 1454 GAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTT 1513
Db 1126 GAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTCACCCAGTTT 1185
Qy 1514 ATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTG 1573
Db 1186 ATTACAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTCCAAAAGGTC 1245
Qy 1574 AACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCCGAT 1633
Db 1246 AACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCGCAACCCGAA 1305
Qy 1634 GAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAGGAC 1693
Db 1306 GACGATATGGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAACCGACAGGAT 1365
Qy 1694 CTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTC 1753
Db 1366 CTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAAGATCAACATA 1425
Qy 1754 GTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGG 1813
Db 1426 ATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGCCAGAGCTGG 1485
Qy 1814 GAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCACACG 1873
Db 1486 GATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGCAACCACACG 1545
Qy 1874 AACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCG 1933
Db 1546 AACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGCCTCGGTTCC 1605
Qy 1934 CAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCG 1993
Db 1606 CAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCACTGCGTGCTGATCGATTCG 1665
Qy 1994 CCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAA 2053
Db 1666 CCAGAGGCACTAAACATGATGCGGGATGAGCACATCAAGGTGATCATCTCCCTGCTGGAG 1725
Qy 2054 AAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGC 2113
Db 1726 AAGCACGGCAGGGACCCGAAAGTCCTAGACGTTCTGTGTTCCTTGTGCGTGGGTAATGGA 1785
Qy 2114 GTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCTG 2173
Db 1786 GTGGCGGTGCGATCCTCCCAGAACAACATTTGCGACTTTTTGCTACCGGGCAAGAATCTG 1845
Qy 2174 TTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGC 2233
Db 1846 TTGCTACAGACGCTCCTGGTGGACCATGTGGCCAGCATCCGACCGAACATCTTCGTGGGT 1905
Qy 2234 CGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCACATA 2293
Db 1906 CGCGTGGACGGTTCTTCCATGTACCAGAAGTGGTACTTCGAGGTGACCATGGATCACATC 1965
Qy 2294 GAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGTTAT 2353
Db 1966 GAACAGACCACGCACATGATGCCCCACCTGCGCATTGGCTGGGCTAATACTTCCGGGTAT 2025
Qy 2354 GTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTGTAC 2413
Db 2026 GTACCGTATCCCGGAGGCGGCAAGAAGTGGGGTGGCAATGGAGTAGGCGATGACCTGTAC 2085
Qy 2414 TCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAATAGG 2473
Db 2086 TCCTTTGGATTTGATGGTGCCTTTCTTTGGACGGGAGGTCGCAAAACACTAGTGGTGGAC 2145
Qy 2474 ACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGACCTG 2533
Db 2146 GCGCTGCCCGAGGAGCCCTTTATCCGTAAAGGCGATGTTATTGGCGTTGCCATTGACCTT 2205
Qy 2534 ACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAAC 2593
Db 2206 TCTGTGCCCATCATCACGTTTACTTTTAACGGAGTAAAAGTGCGCGGTAGCTTTAGGGAC 2265
Qy 2594 TTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGG 2653
Db 2266 TTTAACCTGGACGGAATGTTCTTTCCCGTGATGAGTTGCTCATCAAAACTAAGCTGTCGC 2325
Qy 2654 TTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCCCCG 2713
Db 2326 TTCCTTTTCGGAGGTGATCATGGTCGTTTAAAGTTTGCCCCGCCCATGGGATTCTCTGCC 2385
Qy 2714 CTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGC 2773
Db 2386 CTCGTGCAGTGTCTCATGCCGCAGCAGATCCTCAGTCTGGATCCTTGCTTCTACTTTGGT 2445
Qy 2774 AACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTTGTG 2833
Db 2446 AATCTTGCCAAGAATGTTTTGGCCGGACCATGGCTTATTGAGGACGACACTGCTTTTGTT 2505
Qy 2834 CCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGAGAC 2893
Db 2506 CCGAAGCCCGTTGATACCACGGGTGTGACATTGCCAAGTTCTGTGGACCAAATCAAGGAG 2565
Qy 2894 AAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGGATG 2953
Db 2566 AAGCTGGCGGAGAATATCCACGAGATGTGGGCTCTAAACAAAATCGAGGCGGGCTGGTCG 2625
Qy 2954 TACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAGCGA 3013
Db 2626 TGGGGCGAGCACCGAGATGACTACCACCGCATCCATCCTTGCCTCACCCATTTCGAGAAG 2685
Qy 3014 CTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAGACTATC 3073
Db 2686 CTTCCGGCGGCGGAAAAGCGATACGACAATCAACTAGCTGTGCAAACGCTGAAGACGATT 2745
Qy 3074 CTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTTCGT 3133
Db 2746 ATCTCGCTGGGATACTACATAACCATGGACAAGCCACCAGCACGCATTCGCCCAGTGCGC 2805
Qy 3134 CTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGT 3193
Db 2806 CTGCCCAACGAGATCTTCATGCAGGGCAATGGCTACAAGCCGGCTCCACTTGACCTAAGC 2865
Qy 3194 GCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCAC 3253

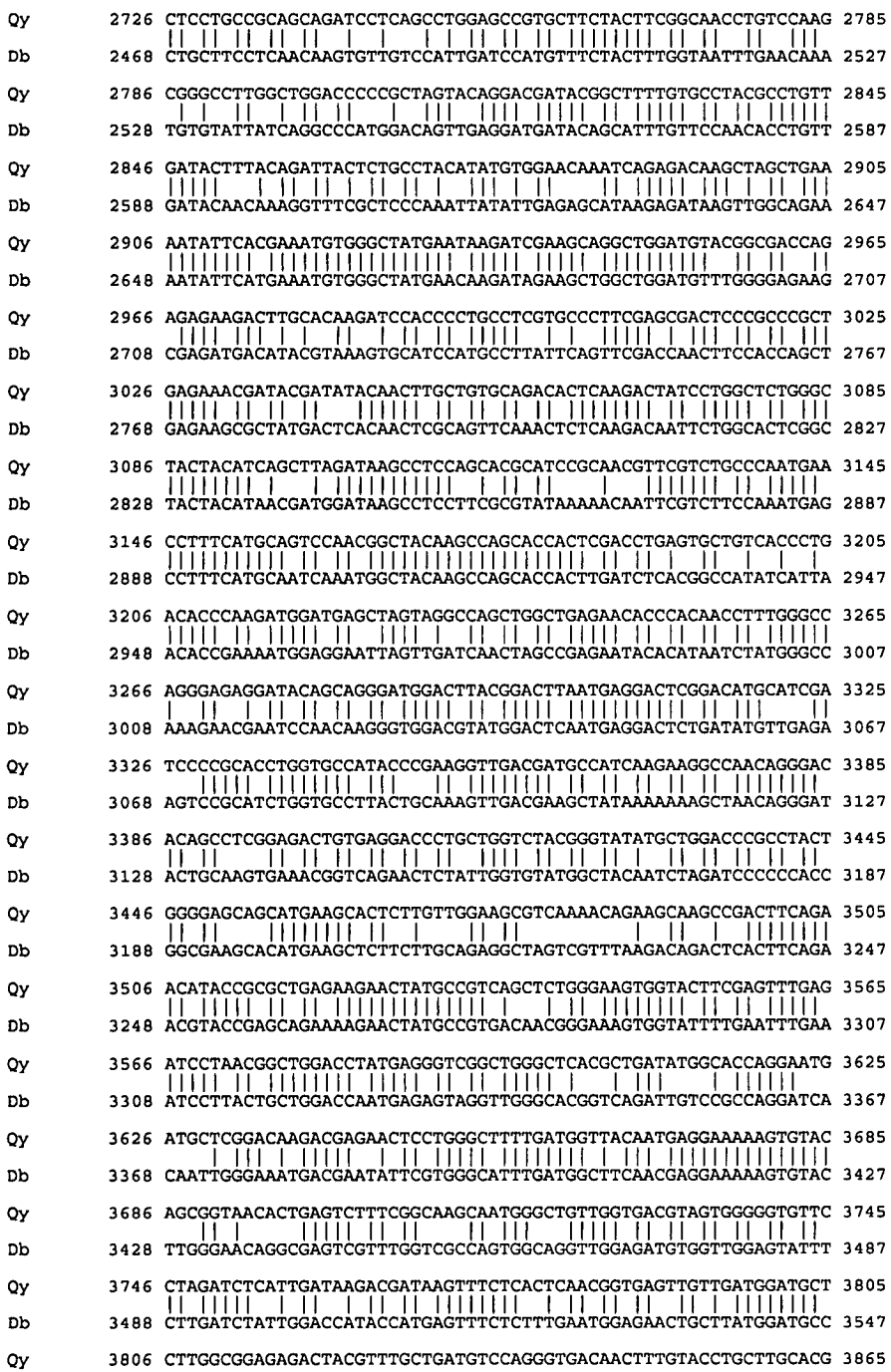


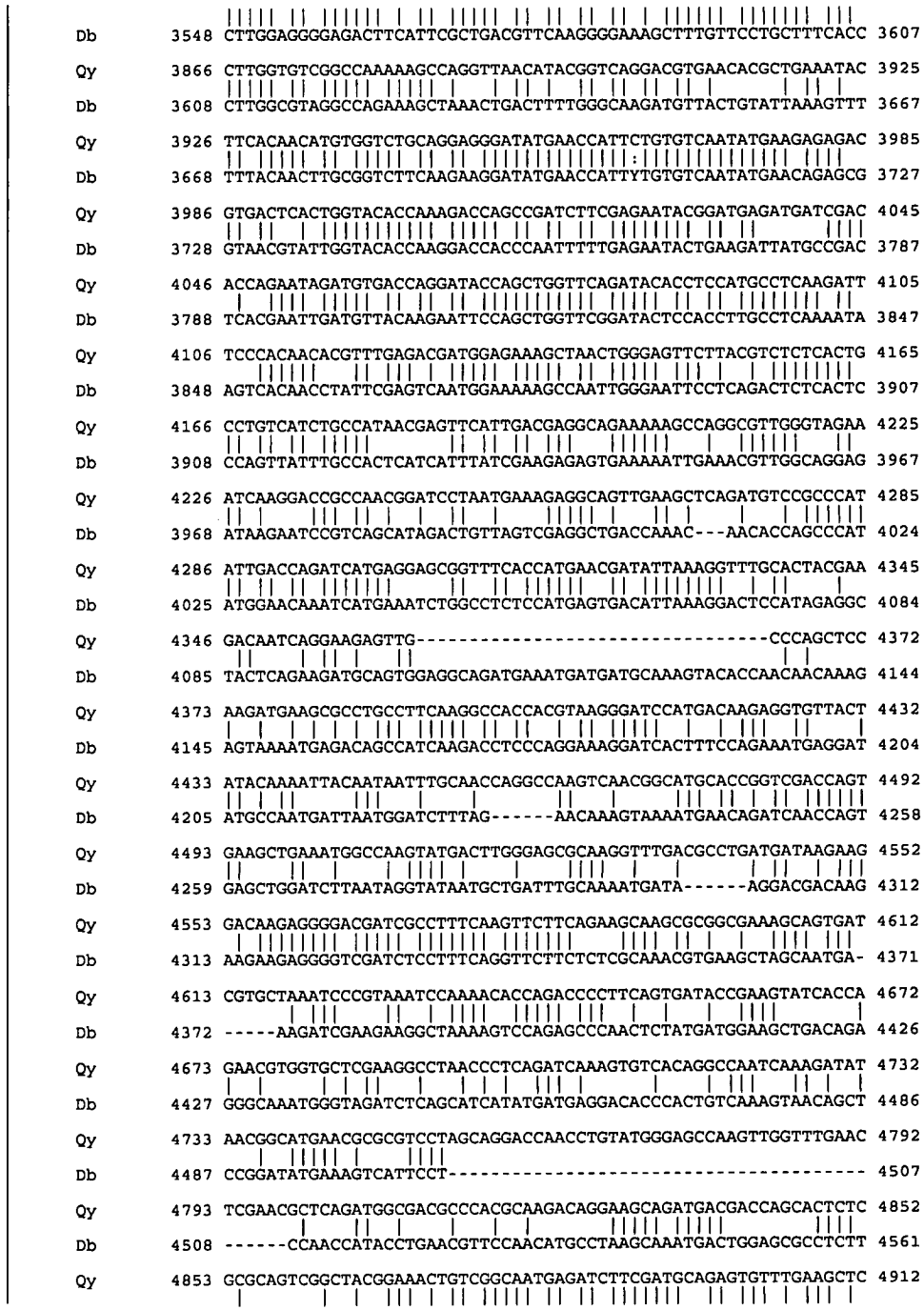


RESULT 8
US-10-668-767-7
; Sequence 7, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 15413
; TYPE: DNA
; ORGANISM: Peregrinus maidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1264)
; OTHER INFORMATION: n = a,c,g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(15397)
; OTHER INFORMATION:
US-10-668-767-7

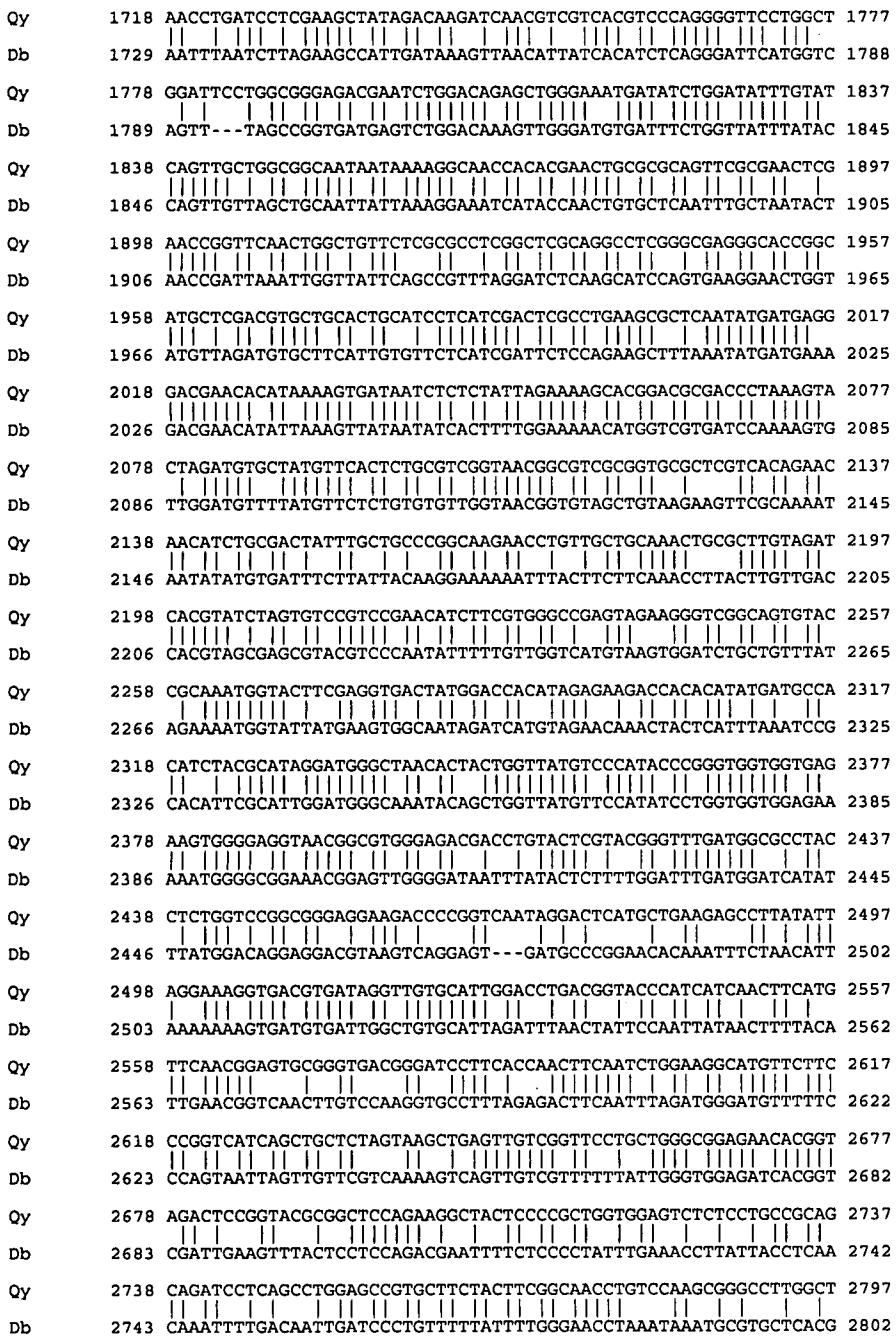
Query Match 41.6%; Score 2078.2; DB 8; Length 15413;
Best Local Similarity 66.5%; Pred. No. 0;
Matches 3172; Conservative 1; Mismatches 1475; Indels 120; Gaps 9;


Db 269 GAA----------GAGGGTAAAGGAACTGGATCAGGACATAGGACCCTATTGTAC 313
Qy 566 GGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTGCCTGTCAACA 625
Db 314 GGCAATGCTATTCTACTTCGGCATCAAAACAGTGATATGTACTTGGCCTGCTCGTCAACC 373
Qy 626 TCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAA 685
Db 374 AGCTCATCCAATGATAAACTGTCATTCGATGTTGGTCTCCAAGAACATTCACAAGGTGAG 433
Qy 686 GCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCGAGAAGGTGCGA 745
Db 434 GCCTGTTGGTGGACTGTGCATCCTGCTTCCAAGCAAAGATCGGAGGGTGAGAAGGTGCGA 493
Qy 746 GTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTGCACACAACGAAA 805
Db 494 GTTGGTGACGACTTGATCTTAGTTTCAGTTGCAACTGAACGATACTTGCATACAACAAAA 553
Qy 806 GAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCACTGGTCGGTACAGCCC 865
Db 554 GAGAACGATTTGTCCATCGTGAATGCTTCCTTTCATGTAACTCATTGGTCCGTTCAGCCT 613
Qy 866 TATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTCGGAGGTGATGTGCTC 925
Db 614 TATGGCACAGGAATAAGTCGCATGAAATATGTTGGTTATGTGTTTGGTGGCGATGTGCTT 673
Qy 926 AGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACTTGGACAAAGGATGGG 985
Db 674 CGGTTCTTTCATGGTGGTGATGAGTGCCTTACAATTCCATCAACGTGGAGTGAAGCACCT 733
Qy 986 GGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCCCGTTCTCTATGG 1045
Db 734 GGACAGAATATTGTGGTTTATGAGGGAGGCAGTGTCATGAGTCAAGCTCGTTCATTATGG 793
Qy 1046 CGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAACTGGTACCATCCTATG 1105
Db 794 AGACTAGAACTTGCTAGAACAAAATGGGCAGGTGGTTTCATAAATTGGTACCACCCAATG 853
Qy 1106 AGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGACCAGAATGAGCTGTAT 1165
Db 854 AGAATACGACACTTGACAACTGGTCGATACCTTGGTGTCAACGAGAACAATGAACTACAT 913
Qy 1166 TTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGCCTGCGCCAGGAGAAG 1225
Db 914 CTGATTGTGAGAGATGAGGCAACGACGGCGTTGTCAGCATTCTGTCTGCGACAAGAGAAA 973
Qy 1226 GATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATAGGCGCGCCCATCATC 1285
Db 974 GATGATCAGAAAGTGGTGCTTGAAGACAAAGACCTAGAAGTAATAGGTGCACCAATTATC 1033
Qy 1286 AAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTGTGGCTGTCTTAT 1345
Db 1034 AAGTATGGTGACAGTACTGTTCTGGTTCAGCATTCTGAGACTGGCTTGTGGCTTACATAC 1093
Qy 1346 AAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTC 1405
Db 1094 AAATCATATGAAACTAAAAAGAAAGGAGTTGGAAAAGTTGAAGAGAAACAAGCTGTGCTC 1153
Qy 1406 CACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGAGGAAGAATCT 1465
Db 1154 CATGAGGAAGGAAAGATGGACGACGGCTTGGATTTCTCCCGCAGTCAAGAAGAAGAATCG 1213
Qy 1466 ATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAATGGCCTG 1525
Db 1214 CGTACCGCTCGTGTAATTAGGAAGTGTTCATCCTTGTTCACTCAGTTTATNAGAGGTCTA 1273
Qy 1526 GAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACCTGGGCGAG 1585
Db 1274 GAGACCTTGCAGGTGAATAGAAGGCACTCGTTATTTTGTGCAACTGTGAATTTGAATGAA 1333
Qy 1586 ATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCCGATGAGGATATGGAA 1645
Db 1334 ATGGTAATGTGCCTCGAAGATTTGATTAACTATTTTGCGCAGCCAGCAGATGATATGGAA 1393
Qy 1646 CACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAGGACCTGTTCCAAGAG 1705
Db 1394 CACGAAGAAAAACAAAATAGGTTCCGTGCATTGAGAAATCGTCAAGATCTGTTTCAAGAA 1453
Qy 1706 GAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCGTCACGTCCCAG 1765
Db 1454 GAAGGCATATTAAATTTAATTCTGGAAGCCATCGATAAAATAAATGTGATAACGTCTCAA 1513
Qy 1766 GGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCT 1825
Db 1514 GGATTCCT---TGTAAGTTTAGCAGGAGATGAATCAGGACAAAGCTGGGATATAATTTCT 1570
Qy 1826 GGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCACACGAACTGCGCGCAG 1885
Db 1571 GGTTACCTGTATCAACTTCTTGCTGCTATAATTAAAGGAAATCATACAAATTGCGCTCAG 1630
Qy 1886 TTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGC 1945
Db 1631 TTTGCGAATTCAAATCGTCTGAATTGGCTGTTCAGCAGACTGGGCTCACAAGCATCAAGT 1690
Qy 1946 GAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAAGCGCTC 2005
Db 1691 GAAGGCACGGGAATGCTTGATGTATTGCATTGTGTTCTCATTGATTCGCCTGAAGCGTTG 1750
Qy 2006 AATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCACGGACGC 2065
Db 1751 AATATGATGAGGGATGAGCATATAAAAGTTATAATATCTCTTCTTGAGAAACATGGAAGG 1810
Qy 2066 GACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGCGTCGCGGTGCGC 2125
Db 1811 GATCCGAAAGTTTTGGATGTTCTCTGTTCACTGTGTGTGGGTAATGGTGTTGCTGTTCGT 1870
Qy 2126 TCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCTGTTGCTGCAAACT 2185
Db 1871 AGCTCACAAAACAATATTTGTGATTTCCTTCTACCTGGAAAAAATCTTCTTCCTCAAACG 1930
Qy 2186 GCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGCCGAGTAGAAGGG 2245
Db 1931 CAACTAGTGGATCATGTGGCTAGTGTCCGTCCAAATATATTTGTTGGGCGTGTTGTTGGC 1990
Qy 2246 TCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGACCACA 2305
Db 1991 TCTGCAGTTTATCAAAAATGGTATTTTGAGGTTACCATGGATCACATTGAGCAGACAACA 2050
Qy 2306 CATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGTTATGTCCCATACCCG 2365
Db 2051 CACATGACACCTCACTTGAGAATTGGCTGGGCGAACACTAGTGGATATGTGCCTTATCCT 2110
Qy 2366 GGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTGTACTCGTACGGGTTT 2425
Db 2111 GGAGGAGGTGAAAAGTGGGGTGGAAATGGAGTTGGTGATGATCTTTATTCTTATGGGTTC 2170
Qy 2426 GATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAATAGGACTCATGCTGAA 2485
Db 2171 GATGGCGCGAATTTATGGACAGGAGGACGTAAAACTTGTGT---TCTACCGCATGCGACT 2227
Qy 2486 GAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGACCTGACGGTACCCATC 2545
Db 2228 GAGCCATTCATCAAGAAAGGCGATGTAATTGGAGTGTCTCTAGATTTAACTGTGCCAATC 2287
Qy 2546 ATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAA 2605
Db 2288 ATAACATTTTCATTCAATGGTTCGCCTATTAGGGGCTGCTTCAGAGATTTCAACTATGAT 2347
Qy 2606 GGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGC 2665
Db 2348 GGAATGTTCTTTCCTGTTATAAGTTGCTCGCACAAGCTAAGTTGCCGATTTCTTTTAGGT 2407
Qy 2666 GGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCCCCGCTGGTGGAGTCT 2725
Db 2408 GGAGACCATGGTCGACTGAAATATGTTCCACCAGAAGAATTCTCTCCACTTGTTGAAAGT 2467



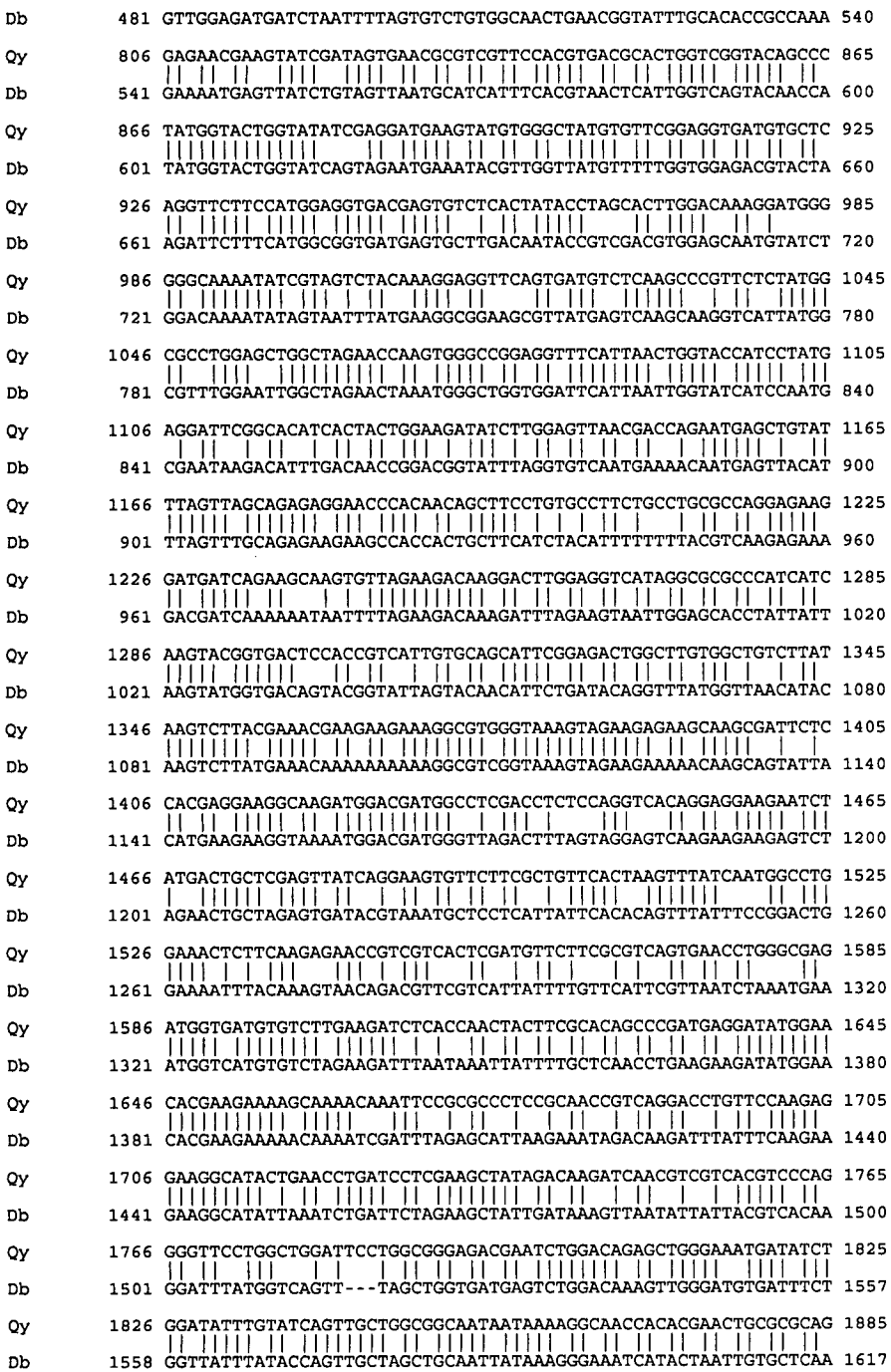


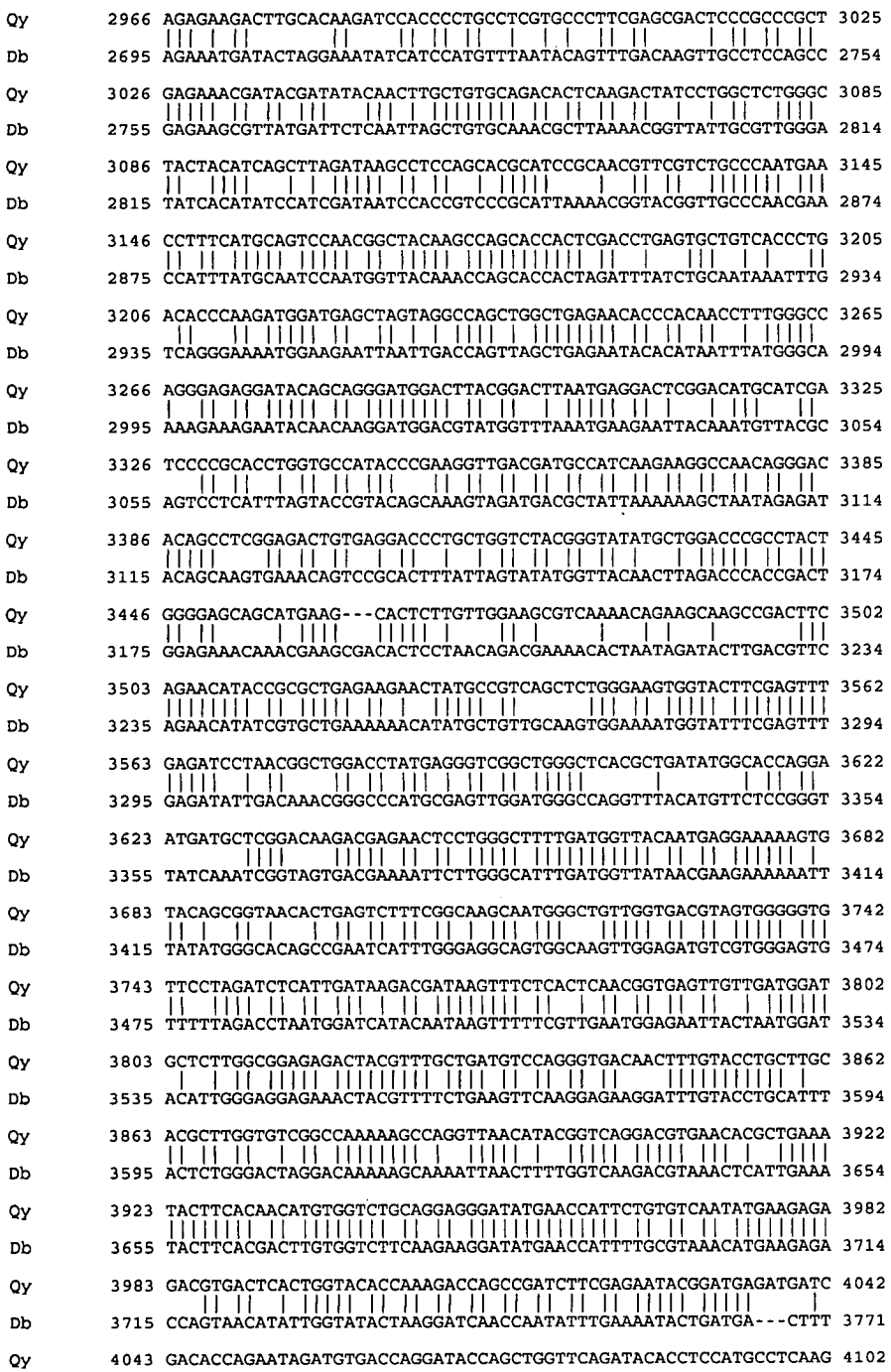
```
Db       4562 TCTGGCAGTGGAATTGAATCGGTTGGCAACGAAATATTCGATGGCGAATGTCTCAAGTTG 4621

Qy       4913 ATCAATGAGTACTTTTATGGAGTCAGGATCTACCCAGGTCAAGACCCAACCCACATGTAC 4972
             |||||||| || || || || ||  | || | ||| ||||| || ||||| ||  ||||
Db       4622 ATCAATGAATATTTCTACGGTGTGCGTATTTTCCCCGGTCAGGATCCAACTCATGTGTAT 4681

Qy       4973 ATCGGCTGGGTGACCACCCAGTACCACT 5000
                 |||| |||||||| ||||||||||||
Db       4682 GTCGGTTGGGTGACAACCCAGTACCACT 4709


RESULT 9
US-10-668-767-3
; Sequence 3, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 15845
;   TYPE: DNA
;   ORGANISM: Myzus persicae
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: (36)..(37)
;   OTHER INFORMATION: n = A, C, G, or T
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5807)
;   OTHER INFORMATION: n = a or t
US-10-668-767-3

  Query Match             36.9%;  Score 1846;  DB 8;  Length 15845;
  Best Local Similarity   63.3%;  Pred. No. 0;
  Matches 2988;  Conservative    0;  Mismatches 1685;  Indels   51;  Gaps    8;

Qy        278 GAGCAAGATGATGTTTCAATCTTGCGTACGGAAGACATGGTGTGCATGTCGTGCACAGCG 337
              || || || ||||| ||  |  | || |||||||| |||||||  | || || || |||
Db        301 GAACAGGACGATGTCTCGTTTCTCCGGACGGAAGATATGGTGTGTTTATCATGTACCGCG 360

Qy        338 ACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCACTGCTTCCTGGAG 397
              || |||||||| || || || || || |||||  | || || ||||| || | | | ||
Db        361 ACCGGAGAGAGAGTTTGTCTTGCAGCAGAAGGATTTGGAAATCGGCATTGTTACTTAGAA 420

Qy        398 AATATTGCCGACAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTTGTCATCGAACAG 457
              |||||||||||  ||||| || || || ||| | || |||||||| |||||||| |||||
Db        421 AATATTGCCGATAAGAATATTCCACCCGATTTATCACAGTGTGTTTTTGTCATTGAACAA 480

Qy        458 GCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAAACTGGGAAA 517
              ||  | || || || |||||||| || || || ||||||||  | ||| ||   || |||
Db        481 GCATTATCTGTGAGGGCTTTACAAGAATTAGTGACAGCTGCAAGTTCTCAAGAGGGAAAA 540

Qy        518 GAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTACGCTACTATACGGCAATGCTATT 577
              |           || || || |||||  | || ||| |||| ||||| |||||||||
Db        541 G------------GCGGAACTGGATCTGGACACCGGACGTTACTGTACGGAAATGCTATT 588

Qy        578 CTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTGCCTGTCAACATCATCATCCCAG 637
                | ||||| ||||  || ||||||||||||  | || || || ||||||   || ||  |

Db        589 TTATTGCGTCATCAAAATAGTGATATGTATTTAGCTTGTCTATCAACAAGTTCTTCAAAT 648

Qy        638 GATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAAGCCTGCTGGTGG 697
              |||||  |  | |||||||| ||| | ||| |||| || |||||||||| || ||||||
Db        649 GATAAATTATCTTTTGACGTTGGTTTACAAGAGCATTCACAAGGTGAAGCTTGTTGGTGG 708

Qy        698 ACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCGAGAAGGTGCGAGTCGGAGATGAC 757
              ||  | ||||||||    || ||  |||| ||||| || || || | ||||||||||||
Db        709 ACTGTTCATCCTGCATCGAACCAACGATCAGAGGGTGAAAAAGTTCCAGTCGGAGATGAT 768

Qy        758 TTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTGCACACAACGAAAGAGAACGAAGTA 817
              || ||| |||| || || || | |||  | || ||||||||  | |||||  |||||  ||
Db        769 TTAATTTTAGTGTCTGTAGCAACTGAACGGTATTTGCACACCGCCAAAGAAAACGAGTTA 828

Qy        818 TCGATAGTGAACGCGTCGTTCCACGTGACGCACTGGTCGGTACAGCCCTATGGTACTGGT 877
              ||  |||| || || || || || || || || ||||| ||||| || ||||||||||||
Db        829 TCTGTAGTTAATGCCTCATTTCATGTAACTCATTGGTCAGTACAACCATATGGTACTGGT 888

Qy        878 ATATCGAGGATGAAGTATGTGGGCTATGTGTTCGGAGGTGATGTGCTCAGGTTCTTCCAT 937
              ||     || ||||| || || || |||||||| || ||||| || || || ||||| |||
Db        889 ATCAGCAGAATGAAATACGTTGGTTATGTGTTTGGTGGTGACGTACTAAGATTCTTTCAT 948

Qy        938 GGAGGTGACGAGTGTCTCACTATACCTAGCACTTGGACAAAGGATGGGGGGCAAAATATC 997
              || || |||||||||  | || |||||      | ||||  || | |   || ||||||||
Db        949 GGCGGCGACGAGTGTTTGACAATACCGTCGTCATGGAGCAATGTTTCTGGACAAAATATA 1008

Qy        998 GTAGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCCCGTTCTCTATGGCGCCTGGAGCTG 1057
              ||| | ||  |||| ||    || |||  ||||||  | ||  |||||||  ||||| ||
Db       1009 GTAATTTATGAAGGCGGAAGCGTTATGAGTCAAGCAAGATCATTATGGCGTTTGGAGTTG 1068

Qy       1058 GCTAGAACCAAGTGGGCCGGAGGTTTCATTAACTGGTACCATCCTATGAGGATTCGGCAC 1117
              |||||||| || |||||||| || |||||||| |||||||||| ||| | ||  | ||
Db       1069 GCTAGAACTAAATGGGCCGGTGGGTTCATTAATTGGTACCATCCAATGCGAATAAGACAT 1128

Qy       1118 ATCACTACTGGAAGATATCTTGGAGTTAACGACCAGAATGAGCTGTATTTAGTTAGCAGA 1177
                | || |||||  | ||| | || || || ||  | |||||  || |||||||| |||||
Db       1129 CTGACAACTGGTCGGTATTTAGGTGTCAATGAAAACAATGAATTGCATTTAGTTTGCAGA 1188

Qy       1178 GAGGAACCCACAACAGCTTCCTGTGCCTTCTGCCTGCGCCAGGAGAAGGATGATCAGAAG 1237
              || ||| |||| || || || | | | || | | | ||||| || || || || || ||
Db       1189 GAAGAAGCCACCACTGCATCTTCTACATTTTTCTTACGCCAAGAAAAAGACGACCAAAAA 1248

Qy       1238 CAAGTGTTAGAAGACAAGGACTTGGAGGTCATAGGCGCGCCCATCATCAAGTACGGTGAC 1297
                | | ||||| ||||| || | || || || || || || || || ||||| ||||||
Db       1249 ATAATTTTAGAGGACAAAGATCTAGAAGTAATTGGTGCACCTATAATTAAGTATGGTGAC 1308

Qy       1298 TCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTGTGGCTGTCTTATAAGTCTTACGAA 1357
                ||| ||  | ||||| ||||| || || || || ||| |  | |||||||||| |||
Db       1309 AGCACAGTGTTAGTGCAACATTCTGATACAGGTTTATGGTTAACATATAAGTCTTATGAA 1368

Qy       1358 ACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTCCACGAGGAAGGC 1417
              || || || ||||| || |||||||||||||| || |||||  |  | ||||| |||||
Db       1369 ACAAAAAAAAAAAGGTGTCGGTAAAGTAGAAGAAAAACAAGCAGTATTACACGAAGAAGGT 1428

Qy       1418 AAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGAGGAAGAATCTATGACTGCTCGA 1477
              |||||||||||||| | ||| |    |||   || || ||||| || | |||||| ||
Db       1429 AAGATGGACGATGGGTTAGACTTTAGTAGGAGTCAAGAAGAAGAGTCAAGAACTGCTAGA 1488

Qy       1478 GTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAATGGCCTGGAAACTCTTCAA 1537
              || ||  | || || |||||  | |||||  |||||||   |||  ||||  |  | |||
Db       1489 GTAATACGCAAATGCTCTTCATTATTCACACAGTTTATTTCTGGATTGGAGAACTTACAA 1548

Qy       1538 GAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGT 1597
                ||| | |||   ||  | || |   |  |  || || ||    || ||||| ||||||
Db       1549 AGTAACAGGCGTTCGTCATTATTTTGTTCATTCGTTAATCTAAATGAAATGGTCATGTGT 1608

Qy       1598 CTTGAAGATCTCACCAACTACTTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAG 1657
              || |||||| |  |  || |||||  || || || || ||||||||||  ||||||||||
Db       1609 CTAGAAGATTTAATAAATTACTTTGCTCAACCTGAAGAGGATATGGAGCACGAAGAAAAA 1668

Qy       1658 CAAAACAAATTCCGCGCCCTCCGCAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTG 1717
              ||||||  |||  | ||  |  | ||  | || ||  | || ||||| ||||| ||| |
Db       1669 CAAAACCGATTTAGAGCATTAAGAAATAGACAAGATTTATTTCAAGAAGAAGGAATATTA 1728
```

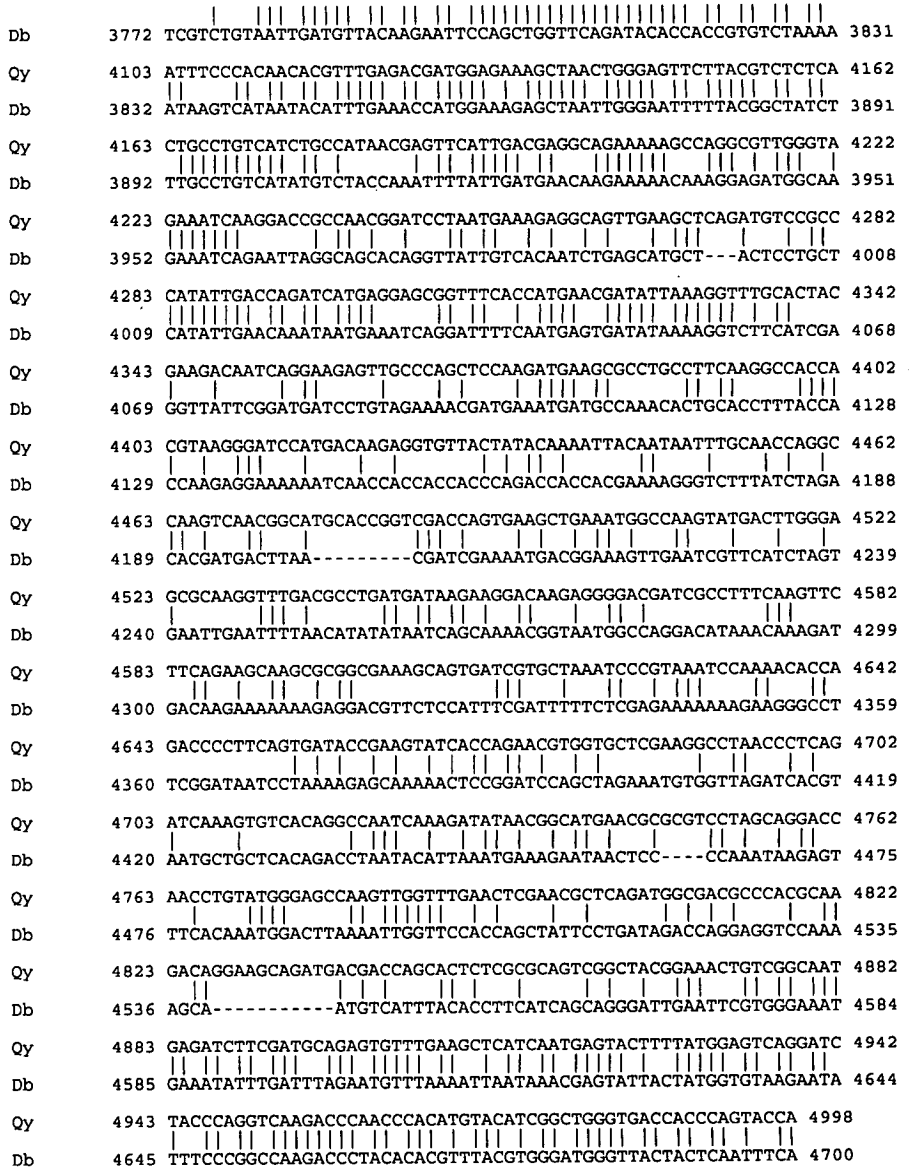

Qy 1718 AACCTGATCCTCGAAGCTATAGACAAGATCAACGTCGTCACGTCCCAGGGGTTCCTGGCT 1777
Db 1729 AATTTAATCTTAGAAGCCATTGATAAAGTTAACATTATCACATCTCAGGGATTCATGGTC 1788
Qy 1778 GGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTAT 1837
Db 1789 AGTT---TAGCCGGTGATGAGTCTGGACAAAGTTGGGATGTGATTTCTGGTTATTTATAC 1845
Qy 1838 CAGTTGCTGGCGGCAATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCG 1897
Db 1846 CAGTTGTTAGCTGCAATTATTAAAGGAAATCATACCAACTGTGCTCAATTTGCTAATACT 1905
Qy 1898 AACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGC 1957
Db 1906 AACCGATTAAATTGGTTATTCAGCCGTTTAGGATCTCAAGCATCCAGTGAAGGAACTGGT 1965
Qy 1958 ATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAAGCGCTCAATATGATGAGG 2017
Db 1966 ATGTTAGATGTGCTTCATTGTGTTCTCATCGATTCTCCAGAAGCTTTAAATATGATGAAA 2025
Qy 2018 GACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCACGGACGCGACCCTAAAGTA 2077
Db 2026 GACGAACATATTAAAGTTATAATATCACTTTTGGAAAAACATGGTCGTGATCCAAAAGTG 2085
Qy 2078 CTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAAC 2137
Db 2086 TTGGATGTTTTATGTTCTCTGTGTGTTGGTAACGGTGTAGCTGTAAGAAGTTCGCAAAAT 2145
Qy 2138 AACATCTGCGACTATTTGCTGCCCGGCAAGAACCTGTTGCTGCAAACTGCGCTTGTAGAT 2197
Db 2146 AATATATGTGATTTCTTATTACAAGGAAAAAATTTACTTCTTCAAACCTTACTTGTTGAC 2205
Qy 2198 CACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTAC 2257
Db 2206 CACGTAGCGAGCGTACGTCCCAATATTTTTGTTGGTCATGTAAGTGGATCTGCTGTTTAT 2265
Qy 2258 CGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGACCACACATATGATGCCA 2317
Db 2266 AGAAAATGGTATTATGAAGTGGCAATAGATCATGTAGAACAAACTACTCATTTAAATCCG 2325
Qy 2318 CATCTACGCATAGGATGGGCTAACACTACTGGTTATGTCCCATACCCGGGTGGTGGTGAG 2377
Db 2326 CACATTCGCATTGGATGGGCAAATACAGCTGGTTATGTTCCATATCCTGGTGGTGGAGAA 2385
Qy 2378 AAGTGGGGAGGTAACGGCGTGGGAGACGACCTGTACTCGTACGGGTTTGATGGCGCCTAC 2437
Db 2386 AAATGGGGCGGAAACGGAGTTGGGGATAATTTATACTCTTTTGGATTTGATGGATCATAT 2445
Qy 2438 CTCTGGTCCGGCGGGAGGAAGACCCCGGTCAATAGGACTCATGCTGAAGAGCCTTATATT 2497
Db 2446 TTATGGACAGGAGGACGTAAGTCAGGAGT---GATGCCCGGAACACAAATTTCTAACATT 2502
Qy 2498 AGGAAAGGTGACGTGATAGGTTGTGCATTGGACCTGACGGTACCCATCATCAACTTCATG 2557
Db 2503 AAAAAAAGTGATGTGATTGGCTGTGCATTAGATTTAACTATTCCAATTATAACTTTTACA 2562
Qy 2558 TTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTC 2617
Db 2563 TTGAACGGTCAACTTGTCCAAGGTGCCTTTAGAGACTTCAATTTAGATGGGATGTTTTTC 2622
Qy 2618 CCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGT 2677
Db 2623 CCAGTAATTAGTTGTTCGTCAAAAGTCAGTTGTCGTTTTTTATTGGGTGGAGATCACGGT 2682
Qy 2678 AGACTCCGGTACGCGGCTCCAGAAGGCTACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAG 2737
Db 2683 CGATTGAAGTTTACTCCTCCAGACGAATTTTCTCCCCTATTTGAAACCTTATTACCTCAA 2742
Qy 2738 CAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCT 2797
Db 2743 CAAATTTTGACAATTGATCCCTGTTTTTATTTTGGGAACCTAAATAAATGCGTGCTCACG 2802
Qy 2798 GGACCCCCGCTAGTACAGGACGATACGGCTTTTGTGCCTACGCCTGTTGATACTTTACAG 2857
Db 2803 GGTCCATGGTATGTTGAAGACGGTACAGCATTTGTTCCAAATCCAGTTGATACTTCGATG 2862
Qy 2858 ATTACTCTGCCTACATATGTGGAACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAA 2917
Db 2863 GTCACCTTGCCTAGTTACATAGAAAATATTAAAGACAAATTAGCAGAGAATATTCACGAA 2922
Qy 2918 ATGTGGGCTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTG 2977
Db 2923 ATGTGGGCAATGAATAAAATTGAAGCTGGTTGGCAATATGGCGATAAAAGAAATGATACT 2982
Qy 2978 CACAAGATCCACCCCTGCCTCGTGCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATAC 3037
Db 2983 AGGAAGTATCATCCATGTTTAATACAGTTTGACAAGTTGCCTCCAGCCGAGAAGCGTTAT 3042
Qy 3038 GATATACAACTTGCTGTGCAGACACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGC 3097
Db 3043 GATTCTCAATTAGCTGTGCAAACGCTTAAAACGGTTATTGCGTTAGGTTATCACATATCT 3102
Qy 3098 TTAGATAAGCCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAG 3157
Db 3103 ATTGATAATCCACCGTCCCGCATTAAAACAGTCCGGCTGCCCAACGAACCATTTATGCAA 3162
Qy 3158 TCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATG 3217
Db 3163 TCCAATGGATATAAACCAGCACCACTAGATTTATCTGCTATCATTTTGTCAGGAAAAATG 3222
Qy 3218 GATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATA 3277
Db 3223 GAAGAACTAATTGATCAGTTAGCCGGGAATACACATAATCTATGGGCAAAAGAAAGAATA 3282
Qy 3278 CAGCAGGGATGGACTTACGGACTTAATGAGGACTCGGACATGCATCGATCCCCGCACCTG 3337
Db 3283 CAGCAAGGATGGACATATGGATTAAATGAAGAATTACAAATGTTGCGCAGTCCTCATTTA 3342
Qy 3338 GTGCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAG 3397
Db 3343 GTACCGTACAGCAAAGTAGACGACGCTATTAAAAAAGCTAATAGAGATACAGCAAGCGAA 3402
Qy 3398 ACTGTGAGGACCCTGCTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCAT 3457
Db 3403 ACAGTCCGCACATTATTGGTATATGGTTACAATTTAGATCCCCCAACTGGAGAAACAAAC 3462
Qy 3458 GAAG---CACTCTTGTTGGAAGCGTCAAAACAGAAGCAAGCCGACTTCAGAACATACCGC 3514
Db 3463 GAAGCGACACTCCTAACAGATGACAACTCTAATAGATATTTGACGTTCAGAACATATCGT 3522
Qy 3515 GCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCCTAACG 3574
Db 3523 GCGGAAAAAACGTATGCCGTTTCTAGTGGAAAATGGTACTTCGAATTTGAGATACTGACA 3582
Qy 3575 GCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGA 3634
Db 3583 AGTGGACCTATGCGGGTTGGATGGGCCAGGTTCACATGTTCCCCGGGTTATCAAATCGGC 3642
Qy 3635 CAAGACGAGAACTCCTGGGCTTTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAAC 3694
Db 3643 AGTGATGAAAATTCTTGGGCATTTGATGGTTATAACGAAGAAAAAATTTACATGGGGACA 3702
Qy 3695 ACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTC 3754
Db 3703 GCCGAATCATTTGGTAGACAGTGGCAAGTTGGAGATGTCGTGGGAGTGTTTTTAGATTTA 3762
Qy 3755 ATTGATAAGACGATAAGTTTCTCACTCAACGGTGAGTTGTTGATGGATGCTCTTGGCGGA 3814
Db 3763 ATGGACCATACAATAAGCTTTTCGATGAACGGAGAATTACTAATGGATACGTTAGGAGGG 3822
Qy 3815 GAGACTACGTTTGCTGATGTCCAGGGTGACAACTTTGTACCTGCTTGCACGCTTGGTGTC 3874
Db 3823 GAAACAACATTCTCTGAAGTCCAAGGAGAAGGATTTGTACCTGCGTTTACGCTGGGACTA 3882
Qy 3875 GGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTGAACACGCTGAAATACTTCACAACA 3934

```
Db       3883 GGACAAAAAGCAAAATTGACATTTGGTCAAGACGTTAACTCATTGAAATACTTCACGACT 3942

Qy       3935 TGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTCAATATGAAGAGAGACGTGACTCAC 3994

Db       3943 TGTGGACTTCAAGAAGGATATGAACCATTCTGTGTAAATATGAAGAGGCCTGTTGCTTAT 4002

Qy       3995 TGGTACACCAAAGACCAGCCGATCTTCGAGAATACGGATGAGATGATCGACACCAGAATA 4054

Db       4003 TGGTATACTAAGGATCAACCAATTTTTGAGAATACTGACGA---TTTTTCGTCTGTTATT 4059

Qy       4055 GATGTGACCAGGATACCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAAC 4114

Db       4060 GATGTTACAAGAATACCAGCTGGTTCAGATACACCACCTTGTCTAAAGATAAGTCATAAT 4119

Qy       4115 ACGTTTGAGACGATGGAGAAAGCTAACTGGGAGTTCTTACGTCTCTCACTGCCTGTCATC 4174

Db       4120 ACATTTGAAACCATGGAAAAAGCCAATTGGGAATTTTTACGGCTATCATTACCTGTCATA 4179

Qy       4175 TGCCATAACGAGTTCATTGACGAGGCAGAAAAAGCCAGGCGTTGGGTAGAAATCAAGGAC 4234

Db       4180 TGTCTACCAAGTTTTATTGGCGATCAAGAAAAACAAAGGGGATGGCAAGAAATAAGAATT 4239

Qy       4235 CGCCAACGGATCCTAATGAAAGAGGCAGTTGAAGCTCAGATGTCCGCCCATATTGACCAG 4294

Db       4240 AGGCAACACAGGTTATTGTCGCAATCTGAGCATGCT---ACTCCTGCTCATATTGAACGA 4296

Qy       4295 ATCATGAGGAGCGGTTTCACCATGAACGATATTAAAGGTTTGCACTACGAAGACAATCAG 4354

Db       4297 ATTATGAAATCAGGATTTTCAATGAGTGATATAAAAGGTCTTCATCGAGGTTATTCAGAT 4356

Qy       4355 GAAGAGTTGCCCAGCTCCAAGATGAAGCGCCTGCCTTCAAGGCCACCACGTAAGGGATCC 4414

Db       4357 GATCCTGTTGAAAATGACGAAATTATGCCAAATACTGCGCCTTTACCACCAAGAGGGAAA 4416

Qy       4415 ATGACAAGAGGTGTTACTATACAAAATTACAATAATTTGCAACCAGGCCAAGTCAACGGC 4474

Db       4417 AATCAACCACCACCACCCAGACCACCACGAAAGGGGTCATTATCGAGGCATGATGACTTA 4476

Qy       4475 ATGCACCGGTCGACCAGTGAAGCTGAAATGGCCAAGTATGACTTGGGAGCGCAAGGTTTG 4534

Db       4477 A---------CAATCGAAAATGATGGGAAATTGAATCGTTCATCTAGTGAACTGAATTTC 4527

Qy       4535 ACGCCTGATGATAAGAAGGACAAGAGGGGACGATCGCCTTTCAAGTTCTTCAGAAGCAAG 4594

Db       4528 AACATATATAATCATCAAAATGGCGATGGTCAGGATATAAACAAAGACGATAAGAAAAAG 4587

Qy       4595 CGCGGCGAAAGCAGTGATCGTGCTAAATCCCGTAAATCCAAAACACCAGACCCCTTCAGT 4654

Db       4588 AGAGGACGTTCTCCATTTCGATTTTTCTCGAGAAAAAAAGAAGGACCCTCAGATAACCCG 4647

Qy       4655 GATACCGAAGTATCACCAGAACGTGGTGCTCGAAGGCCTAACCCTCAGATCAAAGTGTCA 4714

Db       4648 AAAAGAGCAAAAACGCCGGATCCAGCTAGGAATGTAGATAGACCACGAAATGCTGCACAC 4707

Qy       4715 CAGGCCAATCAAAGATATAACGGCATGAACGCGCGTCCTAGCAGGACCAACCTGTATGGG 4774

Db       4708 AGACCTAATACATTAAATGAAAGAGTAACC----------------CCCCAAATAAGAGTT 4752

Qy       4775 AGCCAAGTTGGTTTGAACTCGAACGCTCAGATGGCGACGCCCACGCAAGACAGGAAGCAG 4834

Db       4753 TCACAAATGGATTTAAAACTGGTCCCACCAGCTATTCCTGATAGACCAGGAGGTCCAAAA 4812

Qy       4835 ATGACGACCAGCACTCTCGCGCAGTCGGCTACGGAAACTGTCGGCAATGAGATCTTCGAT 4894

Db       4813 GCGATGTCATTTACACCTACATCAGCAGGAATTGAATTTGTGGGAAATGAAATATTTGAT 4872

Qy       4895 GCAGAGTGTTTGAAGCTCATCAATGAGTACTTTTATGGAGTCAGGATCTACCCAGGTCAA 4954

Db       4873 TTAGAATGTTTAAAATTAATAAATGAGTATTACTATGGTGTAAGAATATTCCCGGGTCAA 4932

Qy       4955 GACCCAACCCACATGTACATCGGCTGGGTGACCACCCAGTACCA 4998

Db       4933 GACCCTACACATGTTTACGTGGGATGGGTTACTACTCAATATCA 4976
```

```
RESULT 10
US-10-668-767-5
; Sequence 5, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15315
;   TYPE: DNA
;   ORGANISM: Periplaneta americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15312)
;   OTHER INFORMATION:
US-10-668-767-5

  Query Match             36.7%;  Score 1835.2;  DB 8;  Length 15315;
  Best Local Similarity   63.2%;  Pred. No. 0;
  Matches 2992;  Conservative    0;  Mismatches 1693;  Indels   51;  Gaps    9;

Qy        266 GGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGCGTACGGAAGACATGGTGTGCATG 325

Db         13 GAGGGAAGTTCGGAACAGGACGATGTGTCGTTTCTCCGGACCGAAGATATGGTGTGTTTA 72

Qy        326 TCGTGCACAGCGACAGGAGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCAC 385

Db         73 TCATGCACTGCGACTGGAGAAAGAGTTTGTCTTGCAGCTGAAGGATTTGGAAATCGGCAC 132

Qy        386 TGCTTCCTGGAGAATATTGCCGACAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTT 445

Db        133 TGTTACTTGGAAAATATTGCCGATAAAAATATTCCACCCGACTTGTCTCAGTGTGTATTT 192

Qy        446 GTCATCGAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCT 505

Db        193 GTCATTGAACAAGCATTATCAGTGAGAGCTTTACAAGAACTAGTTACAGCTACAAGTTCT 252

Qy        506 GAAACTGGGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTACGCTACTATAC 565

Db        253 CAAGAAGGAAAAG------------GTGGAACTGGATCTGGACACCGAACATTGTTGTAT 300

Qy        566 GGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTGCCTGTCAACA 625

Db        301 GGAAATGCTATTTTATTACGTCATCAAAATAGCGATATGTATTTAGCTTGTTTATCAACA 360

Qy        626 TCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAA 685

Db        361 AGTTCGTCAAATGATAAATTATCTTTTGACGTTGGTTTACAAGAGCATTCACAAGGTGAA 420

Qy        686 GCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCGAGAAGGTGCGA 745

Db        421 GCTTGTTGGTGGACTGTGCATCCAGCATCGAAACAACGATCAGAGGGTGAAAAAGTTAGA 480

Qy        746 GTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTGCACACAACGAAA 805
```

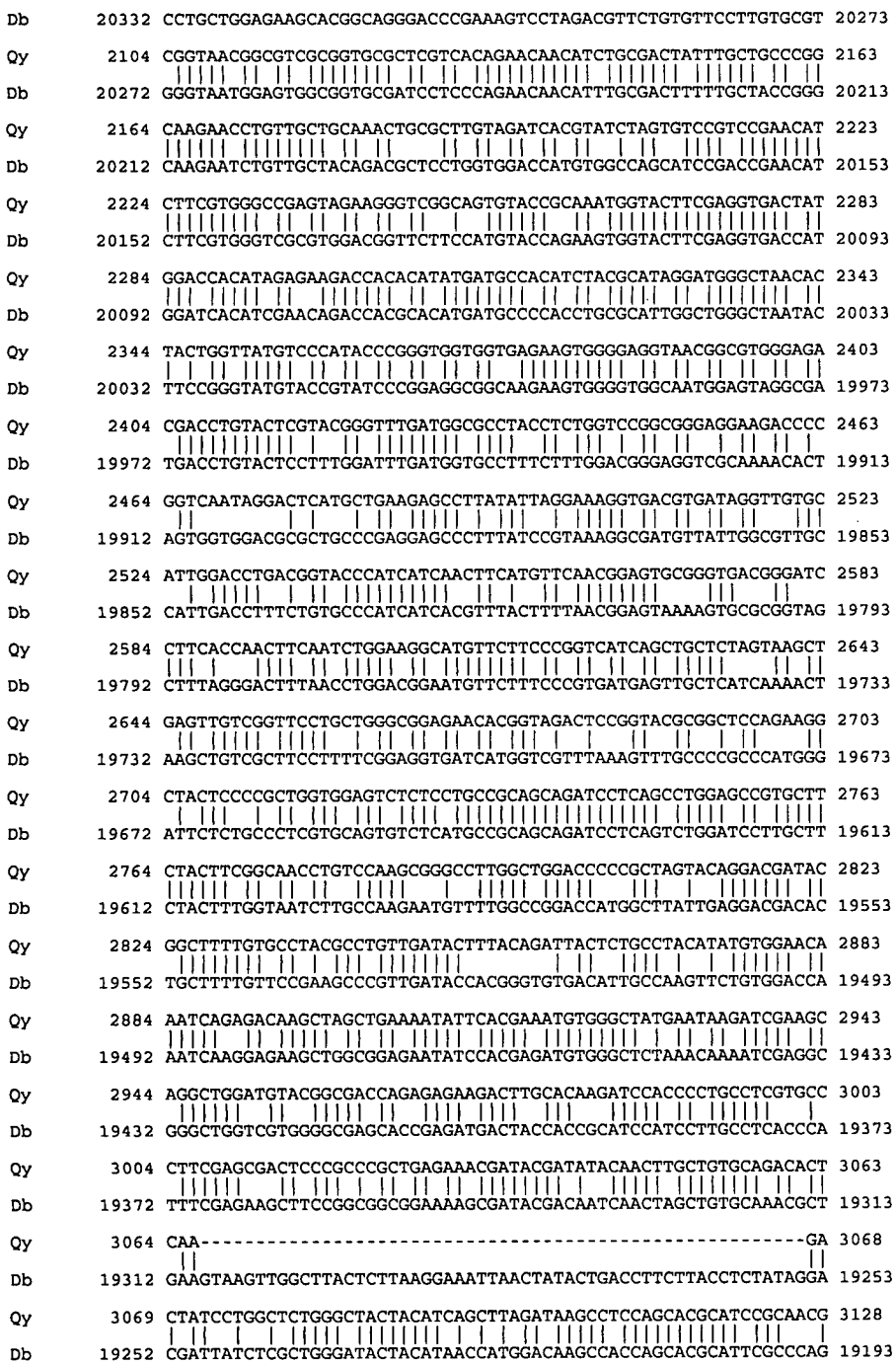

Db 481 GTTGGAGATGATCTAATTTTAGTGTCTGTGGCAACTGAACGGTATTTGCACACCGCCAAA 540
Qy 806 GAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGACGCACTGGTCGGTACAGCCC 865
Db 541 GAAAATGAGTTATCTGTAGTTAATGCATCATTTCACGTAACTCATTGGTCAGTACAACCA 600
Qy 866 TATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTGTTCGGAGGTGATGTGCTC 925
Db 601 TATGGTACTGGTATCAGTAGAATGAAATACGTTGGTTATGTTTTTGGTGGAGACGTACTA 660
Qy 926 AGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACTTGGACAAAGGATGGG 985
Db 661 AGATTCTTTCATGGCGGTGATGAGTGCTTGACAATACCGTCGACGTGGAGCAATGTATCT 720
Qy 986 GGGCAAAATATCGTAGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCCCGTTCTCTATGG 1045
Db 721 GGACAAAATATAGTAATTTATGAAGGCGGAAGCGTTATGAGTCAAGCAAGGTCATTATGG 780
Qy 1046 CGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGTTTCATTAACTGGTACCATCCTATG 1105
Db 781 CGTTTGGAATTGGCTAGAACTAAATGGGCTGGTGGATTCATTAATTGGTATCATCCAATG 840
Qy 1106 AGGATTCGGCACATCACTACTGGAAGATATCTTGGAGTTAACGACCAGAATGAGCTGTAT 1165
Db 841 CGAATAAGACATTTGACAACCGGACGGTATTTAGGTGTCAATGAAAACAATGAGTTACAT 900
Qy 1166 TTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGTGCCTTCTGCCTGCGCCAGGAGAAG 1225
Db 901 TTAGTTTGCAGAGAAGAAGCCACCACTGCTTCATCTACATTTTTTTTACGTCAAGAGAAA 960
Qy 1226 GATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTGGAGGTCATAGGCGCGCCCATCATC 1285
Db 961 GACGATCAAAAAATAATTTTAGAAGACAAAGATTTAGAAGTAATTGGAGCACCTATTATT 1020
Qy 1286 AAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTGTGGCTGTCTTAT 1345
Db 1021 AAGTATGGTGACAGTACGGTATTAGTACAACATTCTGATACAGGTTTATGGTTAACATAC 1080
Qy 1346 AAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTC 1405
Db 1081 AAGTCTTATGAAACAAAAAAAAAAGGCGTCGGTAAAGTAGAAGAAAAACAAGCAGTATTA 1140
Qy 1406 CACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGAGGAAGAATCT 1465
Db 1141 CATGAAGAAGGTAAAATGGACGATGGGTTAGACTTTAGTAGGAGTCAAGAAGAAGAGTCT 1200
Qy 1466 ATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAATGGCCTG 1525
Db 1201 AGAACTGCTAGAGTGATACGTAAATGCTCCTCATTATTCACACAGTTTATTTCCGGACTG 1260
Qy 1526 GAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACCTGGGCGAG 1585
Db 1261 GAAAATTTACAAAGTAACAGACGTTCGTCATTATTTTGTTCATTCGTTAATCTAAATGAA 1320
Qy 1586 ATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCCGATGAGGATATGGAA 1645
Db 1321 ATGGTCATGTGTCTAGAAGATTTAATAAATTATTTTGCTCAACCTGAAGAAGATATGGAA 1380
Qy 1646 CACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAGGACCTGTTCCAAGAG 1705
Db 1381 CACGAAGAAAAACAAAATCGATTTAGAGCATTAAGAAATAGACAAGATTTATTTCAAGAA 1440
Qy 1706 GAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCGTCACGTCCCAG 1765
Db 1441 GAAGGCATATTAAATCTGATTCTAGAAGCTATTGATAAAGTTAATATTATTACGTCACAA 1500
Qy 1766 GGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCT 1825
Db 1501 GGATTTATGGTCAGTT---TAGCTGGTGATGAGTCTGGACAAAGTTGGGATGTGATTTCT 1557
Qy 1826 GGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCACACGAACTGCGCGCAG 1885
Db 1558 GGTTATTTATACCAGTTGCTAGCTGCAATTATAAAGGGAAATCATACTAATTGTGCTCAA 1617
Qy 1886 TTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGC 1945
Db 1618 TTTGCTAACACTAACCGATTAAATTGGTTATTTAGTCGATTAGGATCTCAAGCATCCAGT 1677
Qy 1946 GAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAAGCGCTC 2005
Db 1678 GAGGGAACTGGTATGTTAGATGTACTTCACTGTGTTCTCATTGATTCTCCGGAAGCTTTA 1737
Qy 2006 AATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCACGGACGC 2065
Db 1738 AATATGATGAAAGATGAACATATAAAAGTAATAATATCTCTTTTGGAAAAACATGGTCGT 1797
Qy 2066 GACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGCGTCGCGGTGCGC 2125
Db 1798 GATCCAAAAGTGTTAGACGTTTTATGTTCCCTATGCGTTGGTAACGGTGTGGCCGTAAGA 1857
Qy 2126 TCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCTGTTGCTGCAAACT 2185
Db 1858 AGTTCACAAAATAATATATGTGATTTCTTATTACCAGGAAAAAATTTACTTCTTCAGACC 1917
Qy 2186 GCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGCCGAGTAGAAGGG 2245
Db 1918 TTACTTGTTGATCATGTAGCCAGTGTACGTCCCAATATTTTTGTTGGTCATGTTAGTGGA 1977
Qy 2246 TCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGACCACA 2305
Db 1978 TCTGCCGTTTATCGAAAATGGTATTATGAAGTAGCAATAGATCATGTAGAACAAACTACA 2037
Qy 2306 CATATGATGCCACATCTACGCATAGGATGGGCTAACACTACTGGTTATGTCCCATACCCG 2365
Db 2038 CATTTAAATCCACACATTCGAATTGGATGGGCAAATACTGCAGGTTATGTTCCGTATCCT 2097
Qy 2366 GGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTGTACTCGTACGGGTTT 2425
Db 2098 GGTGGCGGAGAAAAATGGGGTGGAAATGGCGTTGGGGATGATTTATATTCTTTCGGATTT 2157
Qy 2426 GATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAATAGGACTCATGCTGAA 2485
Db 2158 GATGGGTCATATTTATGGACAGGAGGACGTAAATCAGAAGT---GATGCCTGGTTCAGAA 2214
Qy 2486 GAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGACCTGACGGTACCCATC 2545
Db 2215 ATTTCTAACATTAAAAAAGGTGATGTAATCGGTTGTGCATTAGATTTAACTATTCCAATT 2274
Qy 2546 ATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAA 2605
Db 2275 ATAACTTTTACATTGAACGGTCAATTGGTCCAAGGAGCCTTCAGAGACTTCAATTTAGAT 2334
Qy 2606 GGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGC 2665
Db 2335 GGGATGTTTTTCCCAGTAATTAGTTGTTCATCAAAAGTCGGCTGTCGTTTTTTATTGGGC 2394
Qy 2666 GGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCCCCGCTGGTGGAGTCT 2725
Db 2395 GGAGATCATGGTCGATTGAAGTTTACTCCTCCAGACGAATTTTCTCCTCTATTTGAAAGT 2454
Qy 2726 CTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGCAACCTGTCCAAG 2785
Db 2455 TTATTACCTCAACAAATTTTGACAATCGATCCGTGCTTCTATTTTGGAAATCTTAGTAAA 2514
Qy 2786 CGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTTGTGCCTACGCCTGTT 2845
Db 2515 TGCGTACTCACGGGACCGTGGTATGTTGAAGATGATACAGCATTTGTTCCAAATCCAGTT 2574
Qy 2846 GATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGAGACAAGCTAGCTGAA 2905
Db 2575 GATACATCAATGGTCACTTTACCTAGTTACATAGAAAATATTAAAGATAAATTAGCAGAG 2634
Qy 2906 AATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACCAG 2965
Db 2635 AATATTCATGAAATGTGGGCAATGAATAAAATTGAAGCTGGTTGGCAATATGGTGATAAA 2694

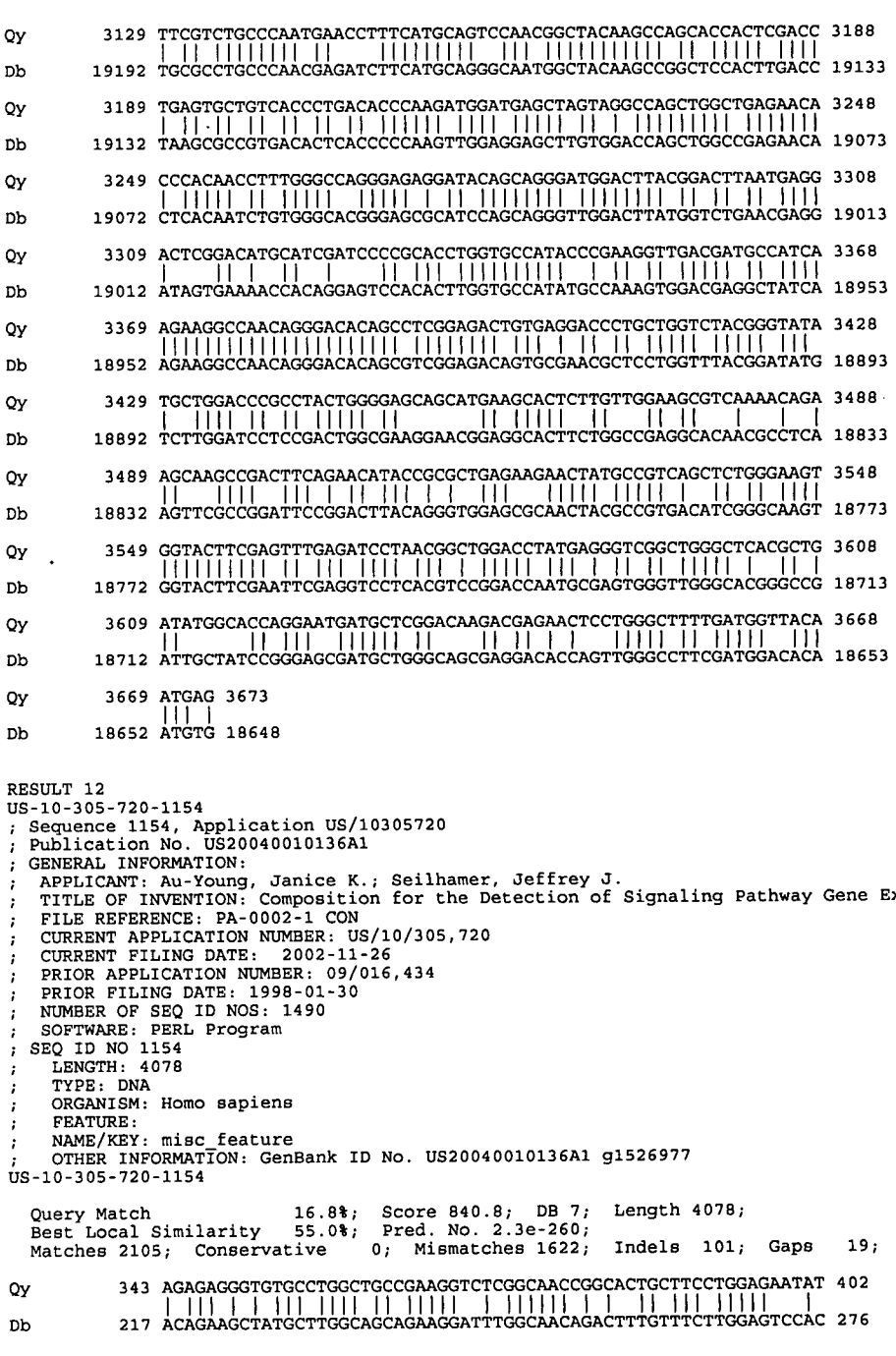




RESULT 11
US-11-097-143-22561/c
; Sequence 22561, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

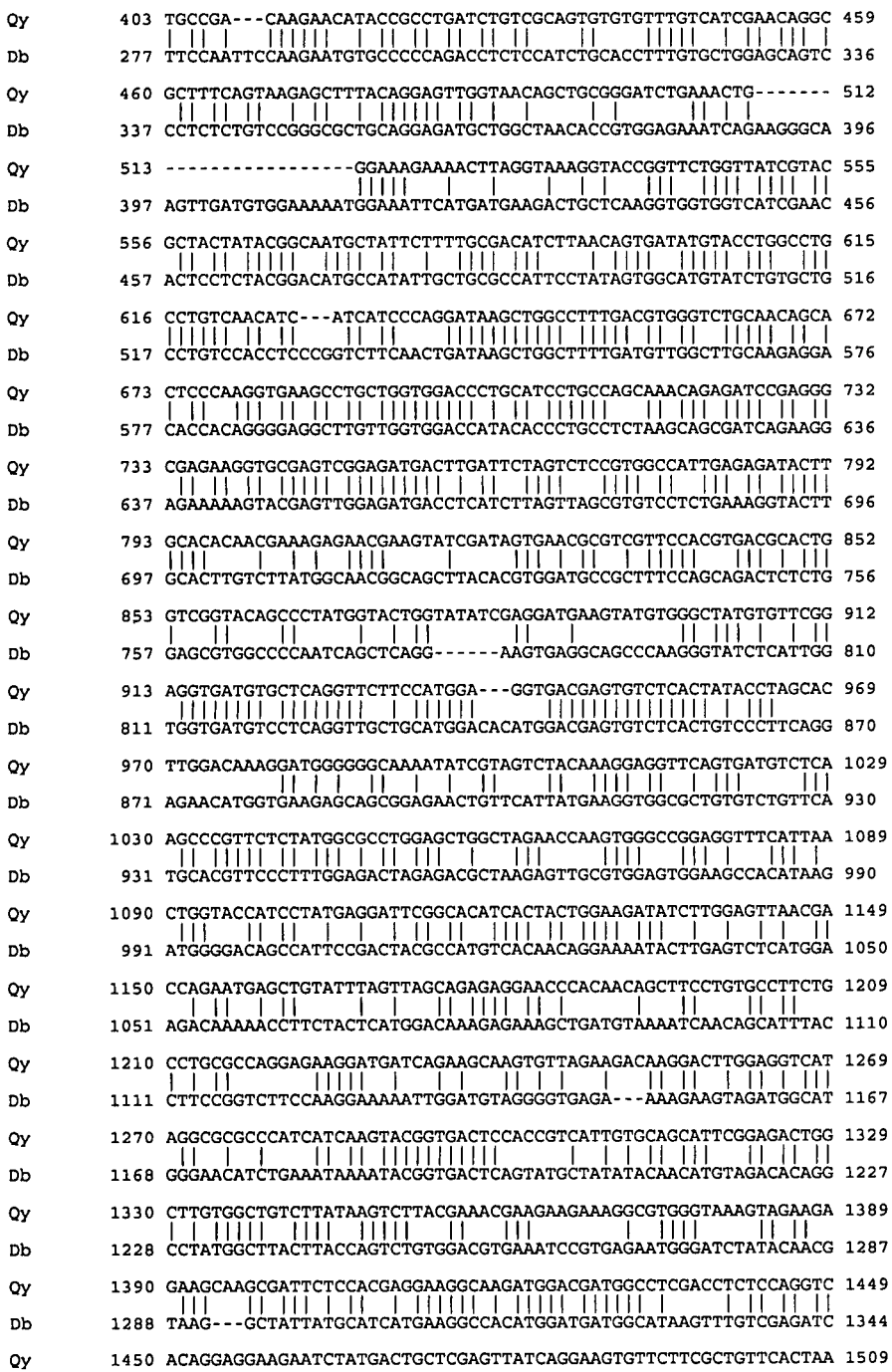
```
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22561
;   LENGTH: 24236
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-22561

  Query Match             29.1%;  Score 1455.8;  DB 13;  Length 24236;
  Best Local Similarity   67.0%;  Pred. No. 0;
  Matches 2256;  Conservative    0;  Mismatches  872;  Indels  237;  Gaps    4;

Qy        546 GTTATCGTACGCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGT 605
              ||  | |  |||| | |   ||| |           |   |||   | ||| |     ||
Db      22012 GTACTTGATCGCTTCCACTTGGCCAGCAAGAATAAATCTAACAATCTTACACTTTGCAGT 21953

Qy        606 ACCTGGCCTGCCTGTCAACATCATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGC 665
              || |||| || ||||| || || || ||  | || |||||| |||| |||||||| ||||
Db      21952 ACTTGGCATGTCTGTCCACCTCCTCGTCGAACGACAAGCTGTCCTTCGACGTGGGCCTGC 21893

Qy        666 AACAGCACTCCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGAT 725
              |  |||||  ||| || || || || ||||||||  | ||||| || ||||| ||| | |
Db      21892 AGGAGCACAGCCAGGGAGAGGCTTGTTGGTGGACGGTTCATCCGGCGAGCAAGCAGCGCT 21833

Qy        726 CCGAGGGCGAGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGA 785
              | |||||||||||||||||| ||||||||||   |||| || || ||||||||||   ||
Db      21832 CTGAGGGCGAGAAGGTGCGCGTCGGAGATGATCTGATCCTGGTGTCCGTGGCCACCGAAC 21773

Qy        786 GATACTTGCACACAACGAAAGAGAACGAAGTATCGATAGTGAACGCGTCGTTCCACGTGA 845
              | || ||||| || || || |||||||||    || || || || ||     ||||| ||||
Db      21772 GTTATTTGCATACGACCAAGGAGAACGAACAGTCTATTGTAAATGCCAGCTTCCATGTGA 21713

Qy        846 CGCACTGGTCGGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATG 905
              | |||||||| || |||||||| || || || || || ||||||||||| ||||||||||
Db      21712 CCCACTGGTCCGTGCAGCCCTACGGCACGGGCATCTCCAGGATGAAGTACGTGGGCTATG 21653

Qy        906 TGTTCGGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTA 965
              | || || || |||||||   | |||||||||||| || |||||||| || || |||| |
Db      21652 TCTTTGGCGGCGATGTGCTGCGTTTCTTCCATGGTGGCGACGAGTGCCTGACCATACCGA 21593

Qy        966 GCACTTGGACAAAGGATGGGGGGCAAAA------------------------------ 993
              | || |||      || | ||| |||||
Db      21592 GTACATGGGGTCGTGAGGCGGGACAAAAGTAAGTTTATCACTCGAAATGACTTAAGTCAC 21533

Qy        994 -------------------------------TATCGTAGTCTACAAAGGAGGTTCAGTG 1021
                                            ||| ||  | ||| | || ||    ||
Db      21532 TATACTAAAGTACCCTTTCAATCCCCTGACAGTATTGTTATTTACGAGGGCGGCGTGGTC 21473

Qy       1022 ATGTCTCAAGCCCGTTCTCTATGGCGCCTGGAGCTGGCTAGAACCAAGTGGGCCGGAGGT 1081
              ||| | || ||  | || || |||||||||||| || ||| |||||||||||| | || ||
Db      21472 ATGGCACAGGCGAGGTCCCTGTGGCGCCTGGAACTCGCTCGAACCAAGTGGACTGGTGGC 21413

Qy       1082 TTCATTAACTGGTACCATCCTATGAGGATTCGGCACATCACTACTGGAAGATATCTTGGA 1141

Db      21412 TTTATCAACTGGTACCACCCGATGCGCATACGCCACATAACCACTGGACGCTACTTGGGC 21353

Qy       1142 GTTAACGACCAGAATGAGCTGTATTTAGTTAGCAGAGAGGAACCCACAACAGCTTCCTGT 1201
              ||  ||||||   || || |||  | ||||||  |  |||||  |  | |  ||  |
Db      21352 GTCAACGACAGCAACGAACTGATTCTAGTTAAGAAGGAGGAGGCTTCGATTGCCACGACG 21293

Qy       1202 GCCTTCTGCCTGCGCCAGGAGAAGGATGATCAGAAGCAAGTGTTAGAAGACAAGGACTTG 1261
              | |||||||||| ||||| ||||| ||  ||||  | ||| | || |||||||| ||
Db      21292 ACTTTCTGCCTGCGGCAGGAAAAGGACGACGAGAAAAAGGTGCTGGAGGACAAGGACCTG 21233

Qy       1262 GAGGTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCG 1321
              ||||| || ||| |||| |||||||||||||| ||| | |||||||| || ||||| |
Db      21232 GAGGTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGC 21173

Qy       1322 GAGACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAA 1381
              |||||| ||||||||||    || |||  ||| || |||| |||| |||| || ||
Db      21172 GAGACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAG 21113

Qy       1382 GTAGAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTC 1441
              || || |||||||||||||| || |||||||| |||||||||||||| | |||||| ||
Db      21112 GTGGAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTC 21053

Qy       1442 TCCAGGTCACAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTG 1501
              ||  | || |||||||| || || | ||| ||||| || ||| | |||||        ||
Db      21052 TCGCGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTC 20993

Qy       1502 TTCACTAAGTTTA---------------------------------------------- 1514
              |||||  ||||||
Db      20992 TTCACCCAGTTTATTACGTAGGTGACTTGGAAGTCCTTTACGAGTGATTTTCTTATCGTA 20933

Qy       1515 ------------TCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCT 1562
                         |||  | | |||||| || ||    || || || ||||| || ||||
Db      20932 TTCACACTCATTTCAGAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCT 20873

Qy       1563 TCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCG 1622
              ||      || |||||   |||||||| ||||| ||||| ||  | |  ||||||||
Db      20872 TCCAAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTT 20813

Qy       1623 CACAGCCCGATGAGGATATG------------------------------------- 1642
              | || ||||| || ||||||
Db      20812 CGCAACCCGAAGACGATATGGGTAAGGTCATTCAAAATATGACCCTAAGATGTTCAATAA 20753

Qy       1643 -------------------GAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAA 1683
                                || ||||| || || || |||  |||||| ||||| |||||
Db      20752 AATCTATAACTAATTTTCAGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAA 20693

Qy       1684 CCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAA 1743
              ||| ||||| |||||||| ||||| ||| | || || |||||||| || || || |||||
Db      20692 CCGACAGGATCTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAA 20633

Qy       1744 GATCAACGTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGG 1803
              ||||||| |  |||| || ||||| ||||| ||  | |||||||| || ||||  | ||
Db      20632 GATCAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGG 20573

Qy       1804 ACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGG 1863
              ||||||||||  | || ||     |||||||| ||  |  |||| || || || || ||
Db      20572 CCAGAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGG 20513

Qy       1864 CAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCG 1923
              |||||||||||||||| ||||||||||   |||||  |||||||| ||||| ||
Db      20512 CAACCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCG 20453

Qy       1924 CCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCT 1983
              |||||| || |||||||| |||||||  |||||||| | ||||| || |||||| | ||
Db      20452 CCTCGGTTCCCAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCACTGCGTGCT 20393

Qy       1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTC 2043
              ||||| |||||  || || || || |||||| |||| || ||||| || |||||  |||||
Db      20392 GATCGATTCGCCAGAGGCACTAAACATGATGCGGGATGAGCACATCAAGGTGATCATCTC 20333

Qy       2044 TCTATTAGAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGT 2103
              ||  | || ||||||||  | ||||| ||||| ||||| || || |||||  | |||||
```

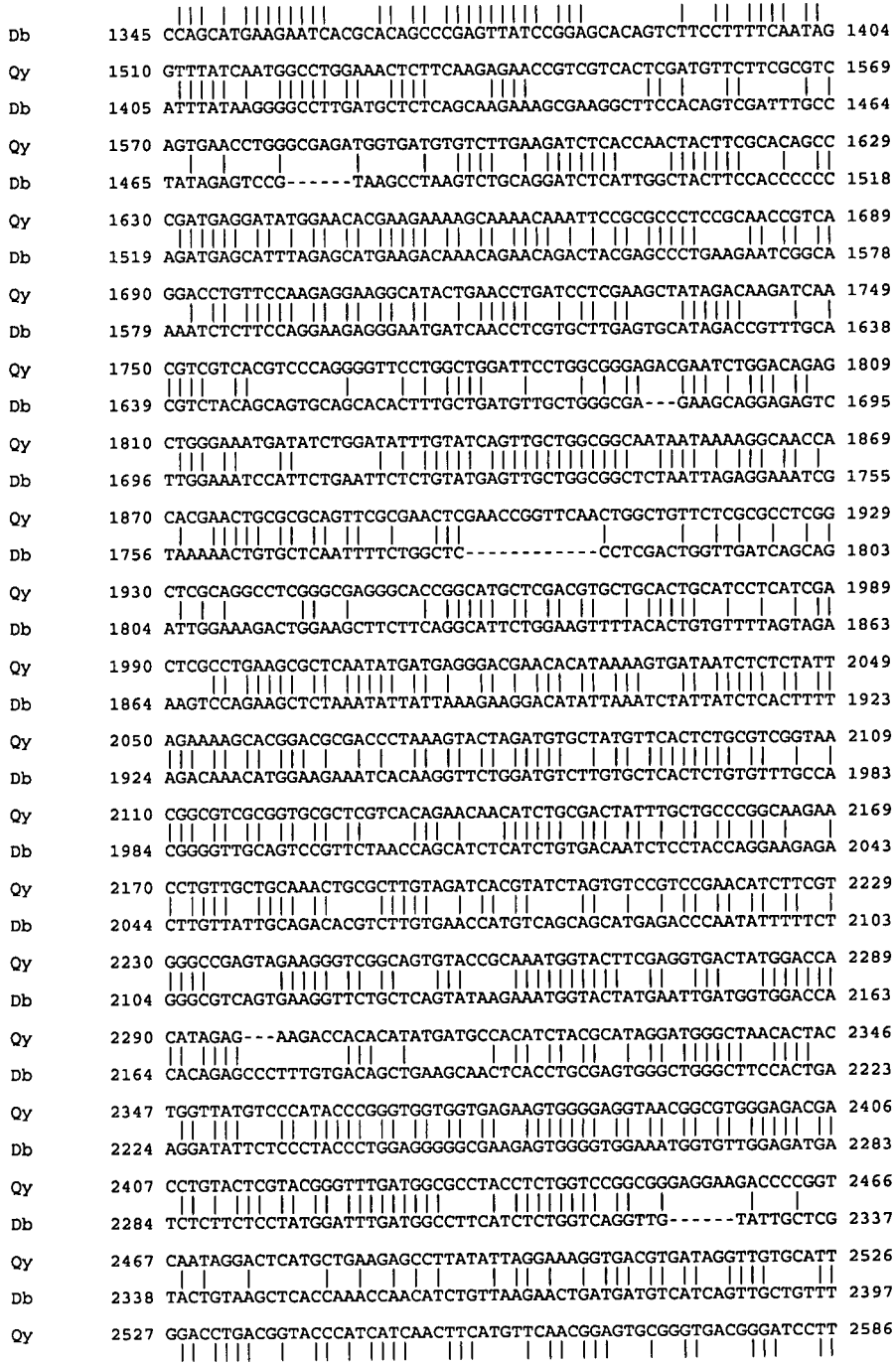




RESULT 12
US-10-305-720-1154
; Sequence 1154, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1154
; LENGTH: 4078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1526977
US-10-305-720-1154

Query Match 16.8%; Score 840.8; DB 7; Length 4078;
Best Local Similarity 55.0%; Pred. No. 2.3e-260;
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;



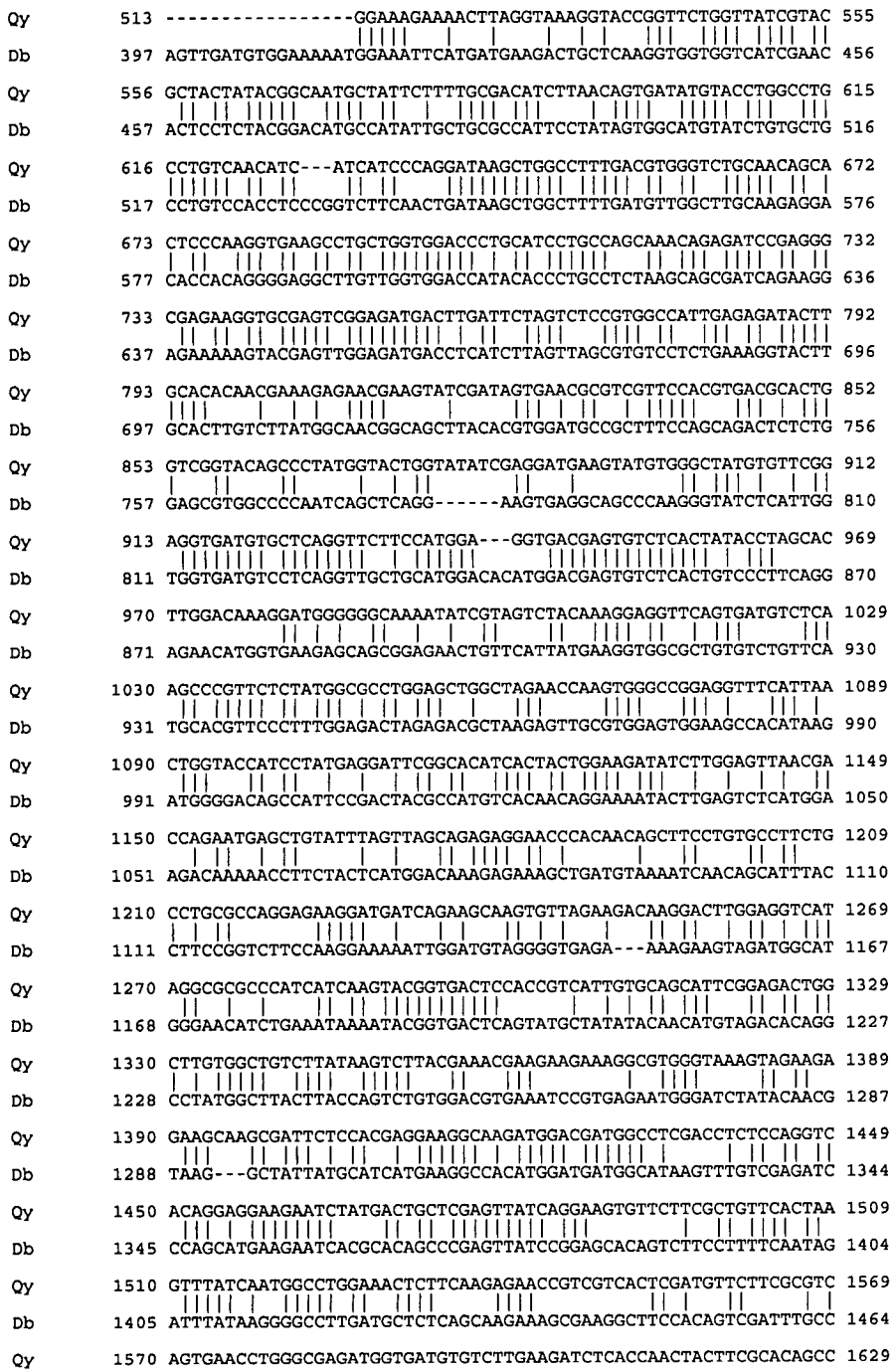


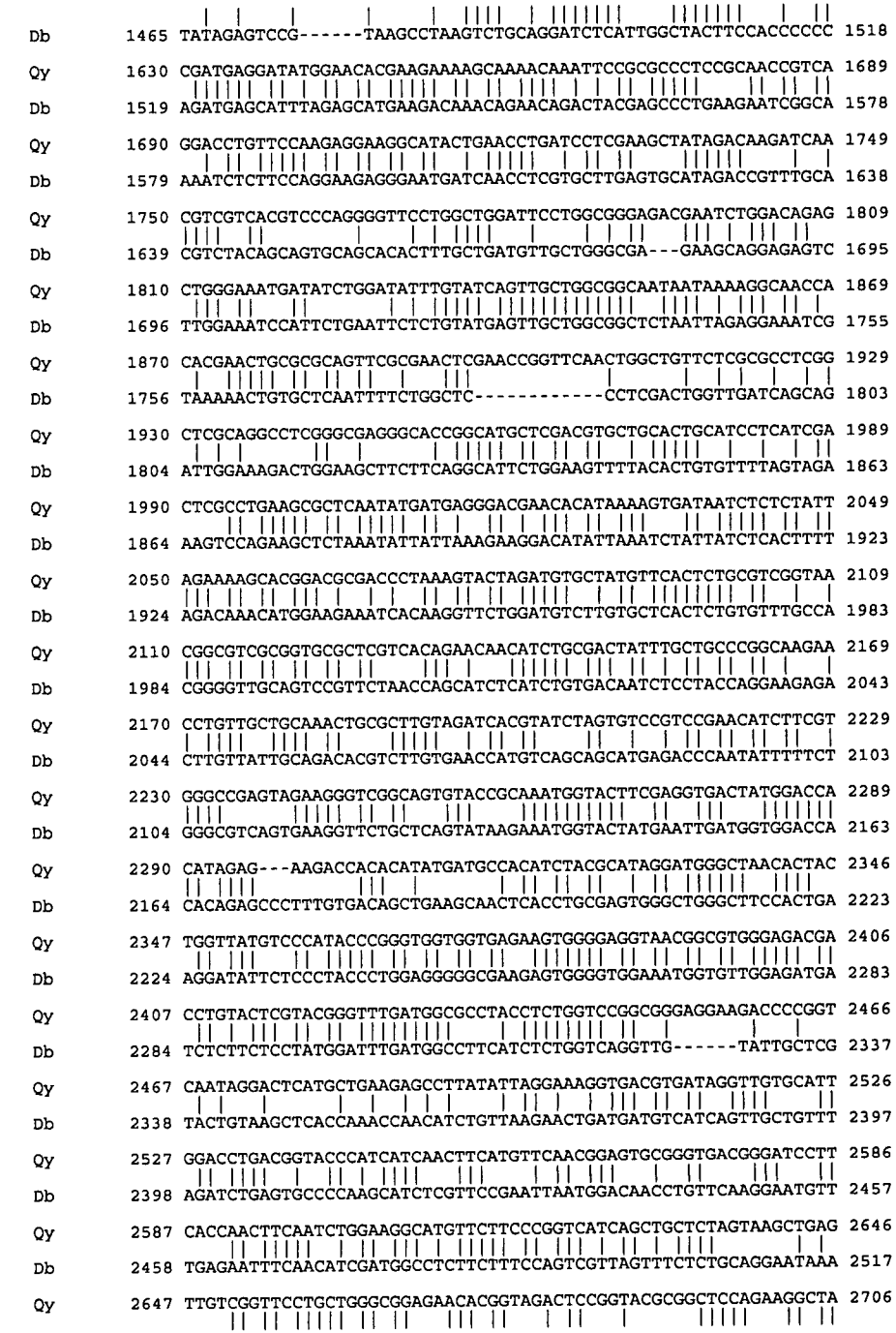
```
Db       2398 AGATCTGAGTGCCCCAAGCATCTCGTTCCGAATTAATGGACAACCTGTTCAAGGAATGTT 2457
Qy       2587 CACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAG 2646
Db       2458 TGAGAATTTCAACATCGATGGCCTCTTCTTTCCAGTCGTTAGTTTCTCTGCAGGAATAAA 2517
Qy       2647 TTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTA 2706
Db       2518 AGTACGCTTTCTGCTTGGAGGGCGACATGGAGAATTCAAATTTCTTCCTCCACCTGGGTA 2577
Qy       2707 CTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGC----- 2761
Db       2578 TGCTCCTTGTTATGAAGCTGTTCTGCCAAAAGAAAAGTTGAAAGTGGAACACAGCCGAGA 2637
Qy       2762 -TTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGA 2820
Db       2638 GTACAAGCAAGAAAGAACTTACACACGCGACCTGCTGGGCCCCACAGTTTCCCTGACGCA 2697
Qy       2821 TACGGCTTTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGA 2880
Db       2698 AGCTGCCTTCACACCCATCCCTGTGGATACCAGCCAGATCGTGTTGCCTCCTCATCTAGA 2757
Qy       2881 ACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGA 2940
Db       2758 AAGAATAAGAGAAAAACTGGCAGAGAATATCCATGAACTCTGGGTTATGAATAAAATTGA 2817
Qy       2941 AGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGT 3000
Db       2818 GCTTGGCTGGCAGTATGGTCCGGTTAGAGATGACAACAAGAGACAACACCCATGCCTGGT 2877
Qy       3001 GCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGAC 3060
Db       2878 GGAGTTCTCCAAGCTGCCTGAACAGGAGCGCAATTACAACTTACAAATGTCGCTTGAGAC 2937
Qy       3061 ACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCAGCACG 3117
Db       2938 CCTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCTGAAGA 2997
Qy       3118 CATCCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGC 3177
Db       2998 CAAGGTGAAAAAAATGAAGCTACCCAAGAATTACCAGCTGACAAGTGGATACAAGCCTGC 3057
Qy       3178 ACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCT 3237
Db       3058 CCCTATGGACCTGAGCTTTATCAAACTCACCCCATCGCAAGAAGCAATGGTGGACAAGTT 3117
Qy       3238 GGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGG 3297
Db       3118 GGCAGAAAATGCACATAATGTGTGGGCGCGGGATCGAATCCGGCAGGGCTGGACTTATGG 3177
Qy       3298 ACTTAATGAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGA 3357
Db       3178 CATCCAACAGGACGTAAAGAACAGAAGAAATCCTCGCCTTGTTCCCTACACTCCTCTGGA 3237
Qy       3358 CGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGT 3417
Db       3238 TGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTGCTGGG 3297
Qy       3418 CTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGC 3477
Db       3298 GTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCCGAAGT 3351
Qy       3478 GTCAAAACAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAG 3537
Db       3352 GTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAA 3411
Qy       3538 CTCTGGGAAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTG 3597
Db       3412 GGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTG 3471
Qy       3598 GGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTT 3657
Db       3472 GAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTT 3531

Qy       3658 TGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATG 3717
Db       3532 TGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGCTCTTG 3588
Qy       3718 GGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTC 3777
Db       3589 GCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATGTTCAC 3648
Qy       3778 ACTCAACGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCA 3837
Db       3649 ACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGACTTTGA 3708
Qy       3838 GGGTGACAA---CTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAAC 3894
Db       3709 TGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGGATGAA 3768
Qy       3895 ATACGGTCAGGACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATA 3954
Db       3769 CTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAGGGCTA 3828
Qy       3955 TGAACCATTCTGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAA-AGACCAGC 4013
Db       3829 TGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGGCTTCC 3888
Qy       4014 CGATCTTCGAGAATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAG 4073
Db       3889 TCAGTTTCTTCAAGTTCCATCAAACCATGAACA----TATAGAGGTGACCAGAATAGACG 3944
Qy       4074 CTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTTG 4121
Db       3945 GCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
```

RESULT 13
US-10-276-774-552
; Sequence 552, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 552
; LENGTH: 14302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-552

Query Match 16.8%; Score 840.8; DB 8; Length 14302;
Best Local Similarity 55.0%; Pred. No. 5e-260;
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;

```
Qy        343 AGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCACTGCTTCCTGGAGAATAT 402
Db        217 ACAGAAGCTATGCTTGGCAGCAGAAGGATTTGGCAACAGACTTTGTTTCTTGGAGTCCAC 276
Qy        403 TGCCGA---CAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTTGTCATCGAACAGGC 459
Db        277 TTCCAATTCCAAGAATGTGCCCCCAGACCTCTCCATCTGCACCTTTGTGCTGGAGCAGTC 336
Qy        460 GCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAAACTG------- 512
Db        337 CCTCTCTGTCCGGGCGCTGCAGGAGATGCTGGCTAACACCGTGGAGAAATCAGAAGGGCA 396
```



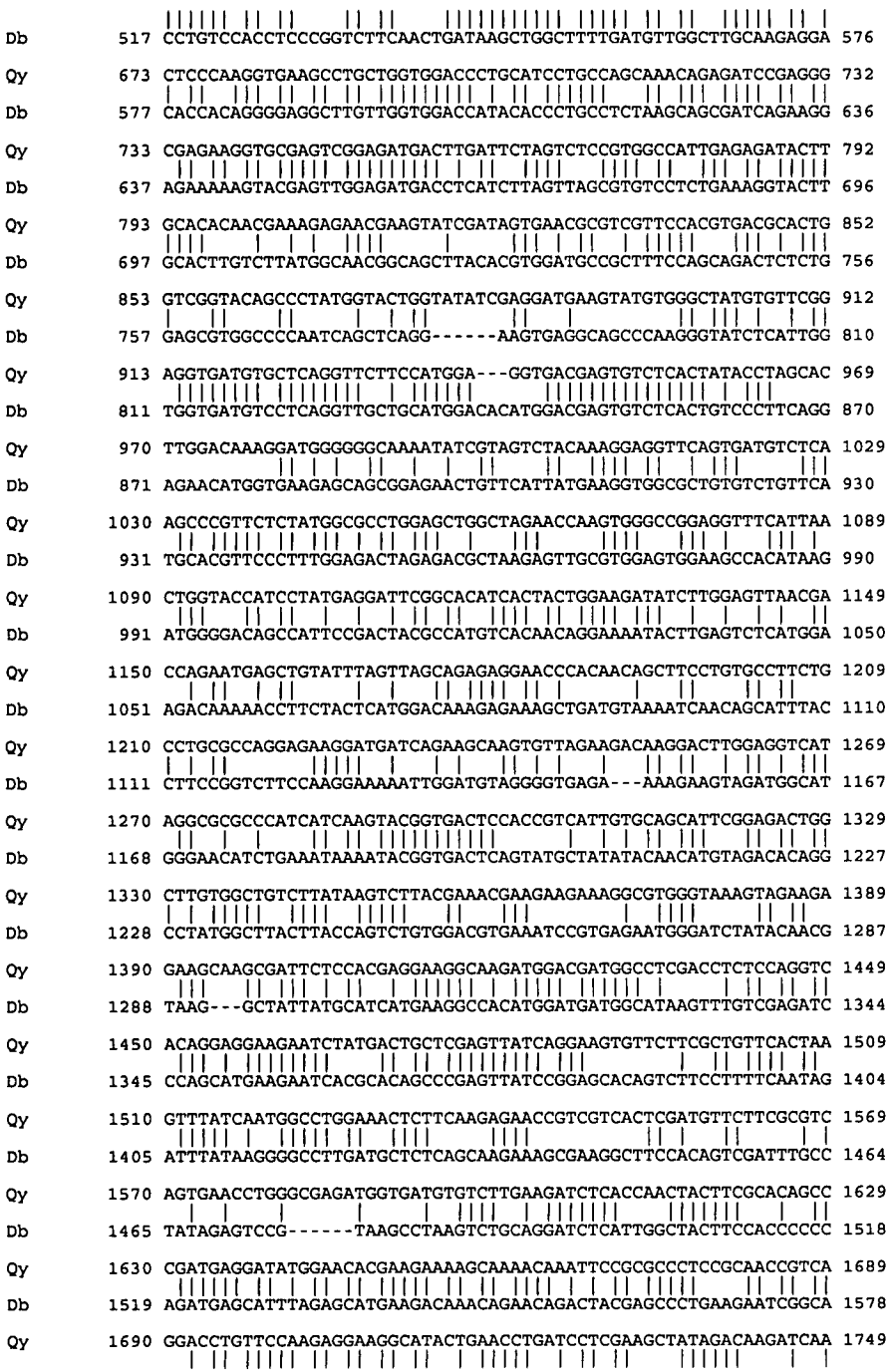


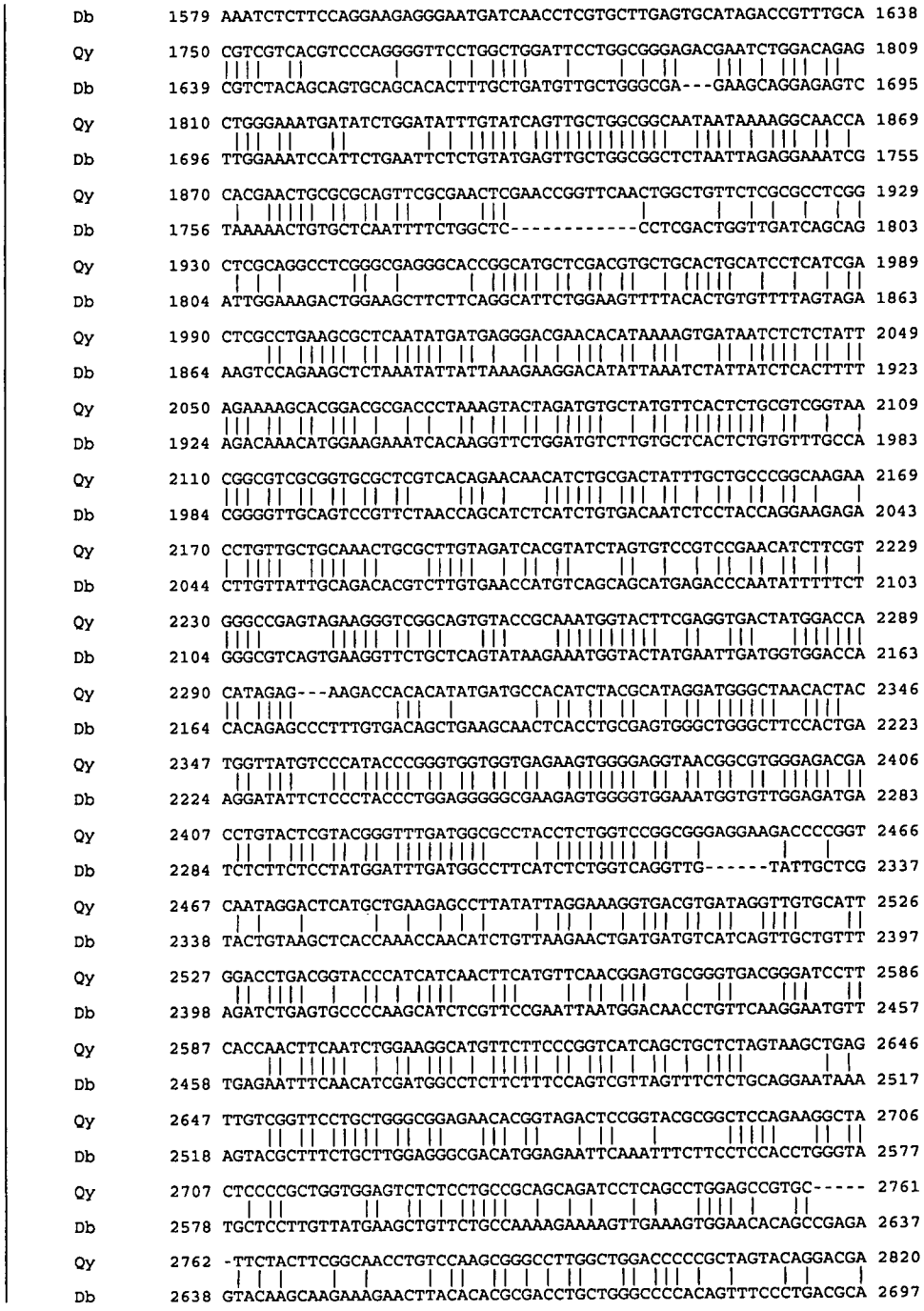
```
Db       2518 AGTACGCTTTCTGCTTGGAGGGCGACATGGAGAATTCAAATTTCTTCCTCCACCTGGGTA 2577
Qy       2707 CTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGC----- 2761
Db       2578 TGCTCCTTGTTATGAAGCTGTTCTGCCAAAAGAAAAGTTGAAAGTGGAACACAGCCGAGA 2637
Qy       2762 -TTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGA 2820
Db       2638 GTACAAGCAAGAAAGAACTTACACACGCGACCTGCTGGGCCCCACAGTTTCCCTGACGCA 2697
Qy       2821 TACGGCTTTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGA 2880
Db       2698 AGCTGCCTTCACACCCATCCCTGTGGATACCAGCCAGATCGTGTTGCCTCCTCATCTAGA 2757
Qy       2881 ACAAATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGA 2940
Db       2758 AAGAATAAGAGAAAAACTGGCAGAGAATATCCATGAACTCTGGGTTATGAATAAAATTGA 2817
Qy       2941 AGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGT 3000
Db       2818 GCTTGGCTGGCAGTATGGTCCGGTTAGAGATGACAACAAGAGACAACACCCATGCCTGGT 2877
Qy       3001 GCCCTTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGAC 3060
Db       2878 GGAGTTCTCCAAGCTGCCTGAACAGGAGCGCAATTACAACTTACAAATGTCGCTTGAGAC 2937
Qy       3061 ACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCAGCACG 3117
Db       2938 CCTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCTGAAGA 2997
Qy       3118 CATCCGCAACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGC 3177
Db       2998 CAAGGTGAAAAAAATGAAGCTACCCAAGAATTACCAGCTGACAAGTGGATACAAGCCTGC 3057
Qy       3178 ACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCT 3237
Db       3058 CCCTATGGACCTGAGCTTTATCAAACTCACCCCATCGCAAGAAGCAATGGTGGACAAGTT 3117
Qy       3238 GGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGG 3297
Db       3118 GGCAGAAAATGCACATAATGTGTGGGCGCGGGATCGAATCCGGCAGGGCTGGACTTATGG 3177
Qy       3298 ACTTAATGAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGA 3357
Db       3178 CATCCAACAGGACGTAAAGAACAGAAGAAATCCTCGCCTTGTTCCCTACACTCCTCTGGA 3237
Qy       3358 CGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGT 3417
Db       3238 TGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTGCTGGG 3297
Qy       3418 CTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGC 3477
Db       3298 GTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCCGAAGT 3351
Qy       3478 GTCAAAACAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAG 3537
Db       3352 GTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAA 3411
Qy       3538 CTCTGGGAAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTG 3597
Db       3412 GGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTG 3471
Qy       3598 GGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTT 3657
Db       3472 GAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTT 3531
Qy       3658 TGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATG 3717
Db       3532 TGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGCTCTTG 3588
Qy       3718 GGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTC 3777
Db       3589 GCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATGTTCAC 3648

Qy       3778 ACTCAACGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCA 3837
Db       3649 ACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGACTTTGA 3708
Qy       3838 GGGTGACAA---CTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAAC 3894
Db       3709 TGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGGATGAA 3768
Qy       3895 ATACGGTCAGGACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATA 3954
Db       3769 CTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAGGGCTA 3828
Qy       3955 TGAACCATTCTGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAA-AGACCAGC 4013
Db       3829 TGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGGCTTCC 3888
Qy       4014 CGATCTTCGAGAATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAG 4073
Db       3889 TCAGTTTCTTCAAGTTCCATCAAACCATGAACA----TATAGAGGTGACCAGAATAGACG 3944
Qy       4074 CTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTTG 4121
Db       3945 GCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
```

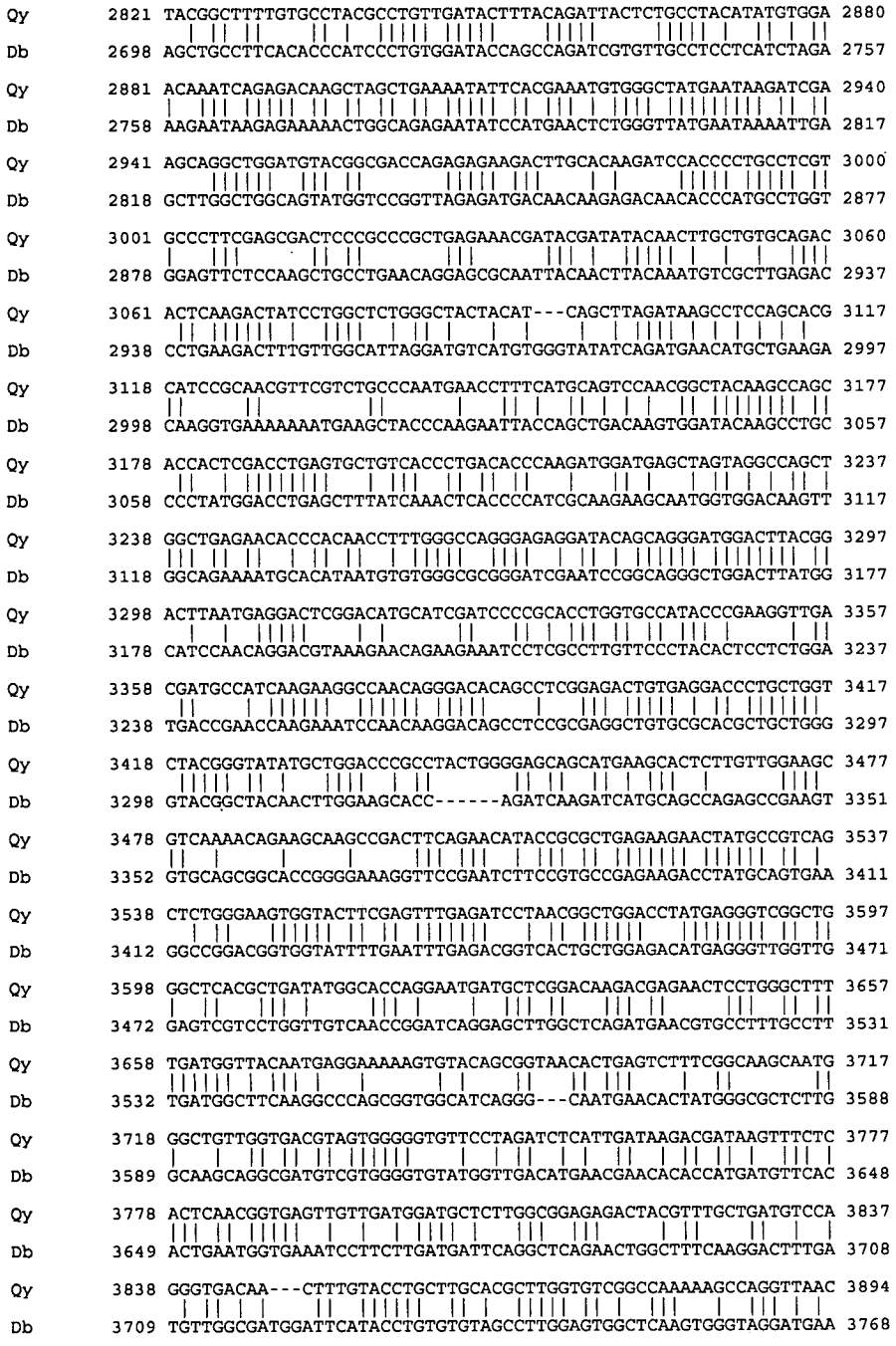
RESULT 14
US-10-887-553A-490
; Sequence 490, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 15731
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-490

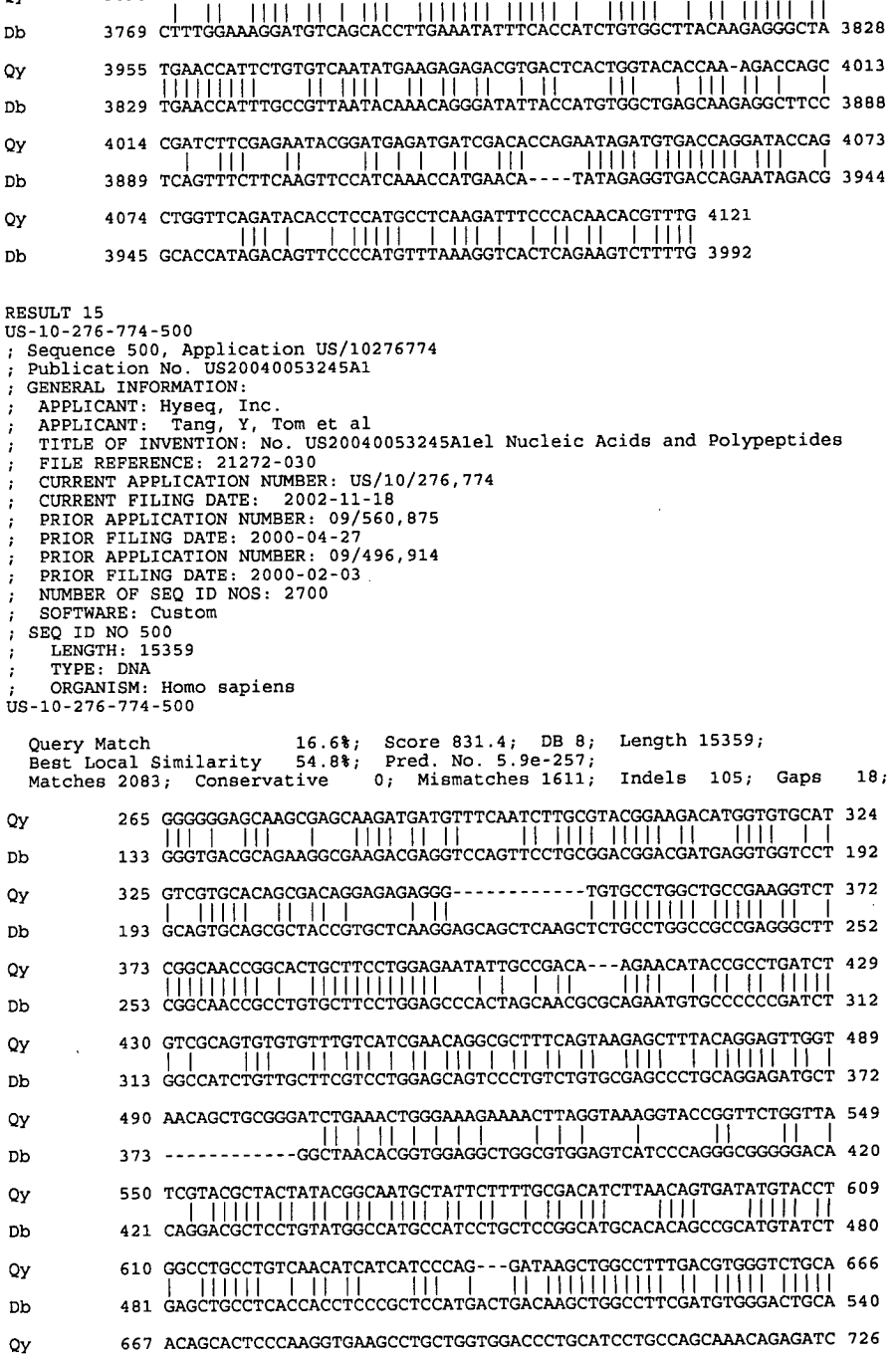
Query Match 16.8%; Score 840.8; DB 10; Length 15731;
Best Local Similarity 55.0%; Pred. No. 5.3e-260;
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;

```
Qy        343 AGAGAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCACTGCTTCCTGGAGAATAT 402
Db        217 ACAGAAGCTATGCTTGGCAGCAGAAGGATTTGGCAACAGACTTTGTTTCTTGGAGTCCAC 276
Qy        403 TGCCGA---CAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTTGTCATCGAACAGGC 459
Db        277 TTCCAATTCCAAGAATGTGCCCCCAGACCTCTCCATCTGCACCTTTGTGCTGGAGCAGTC 336
Qy        460 GCTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAAACTG------- 512
Db        337 CCTCTCTGTCCGGGCGCTGCAGGAGATGCTGGCTAACACCGTGGAGAAATCAGAAGGGCA 396
Qy        513 ----------------GGAAAGAAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTAC 555
Db        397 AGTTGATGTGGAAAAATGGAAATTCATGATGAAGACTGCTCAAGGTGGTGGTCATCGAAC 456
Qy        556 GCTACTATACGGCAATGCTATTCTTTTGCGACATCTTAACAGTGATATGTACCTGGCCTG 615
Db        457 ACTCCTCTACGGACATGCCATATTGCTGCGCCATTCCTATAGTGGCATGTATCTGTGCTG 516
Qy        616 CCTGTCAACATC---ATCATCCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAGCA 672
```



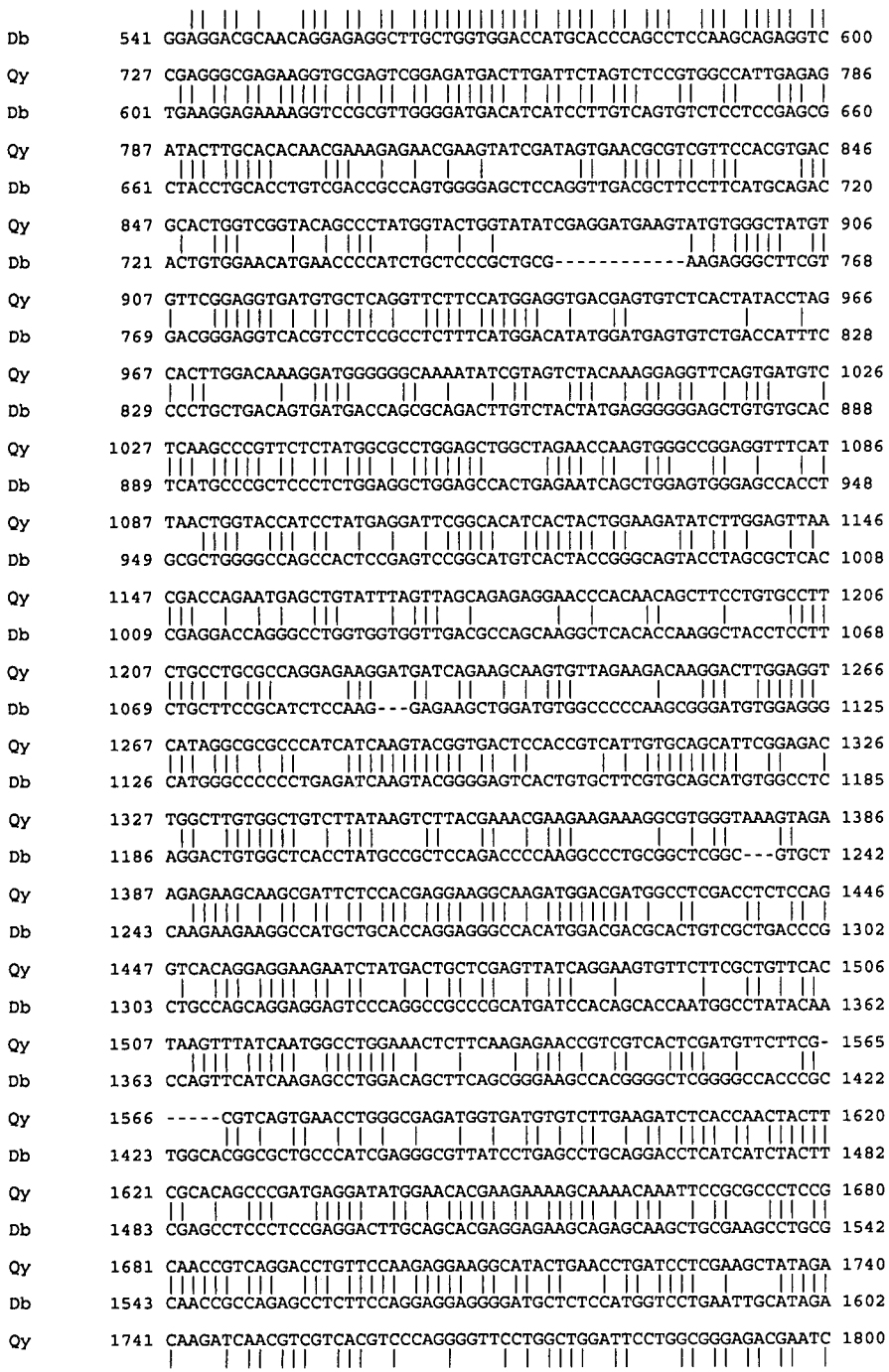


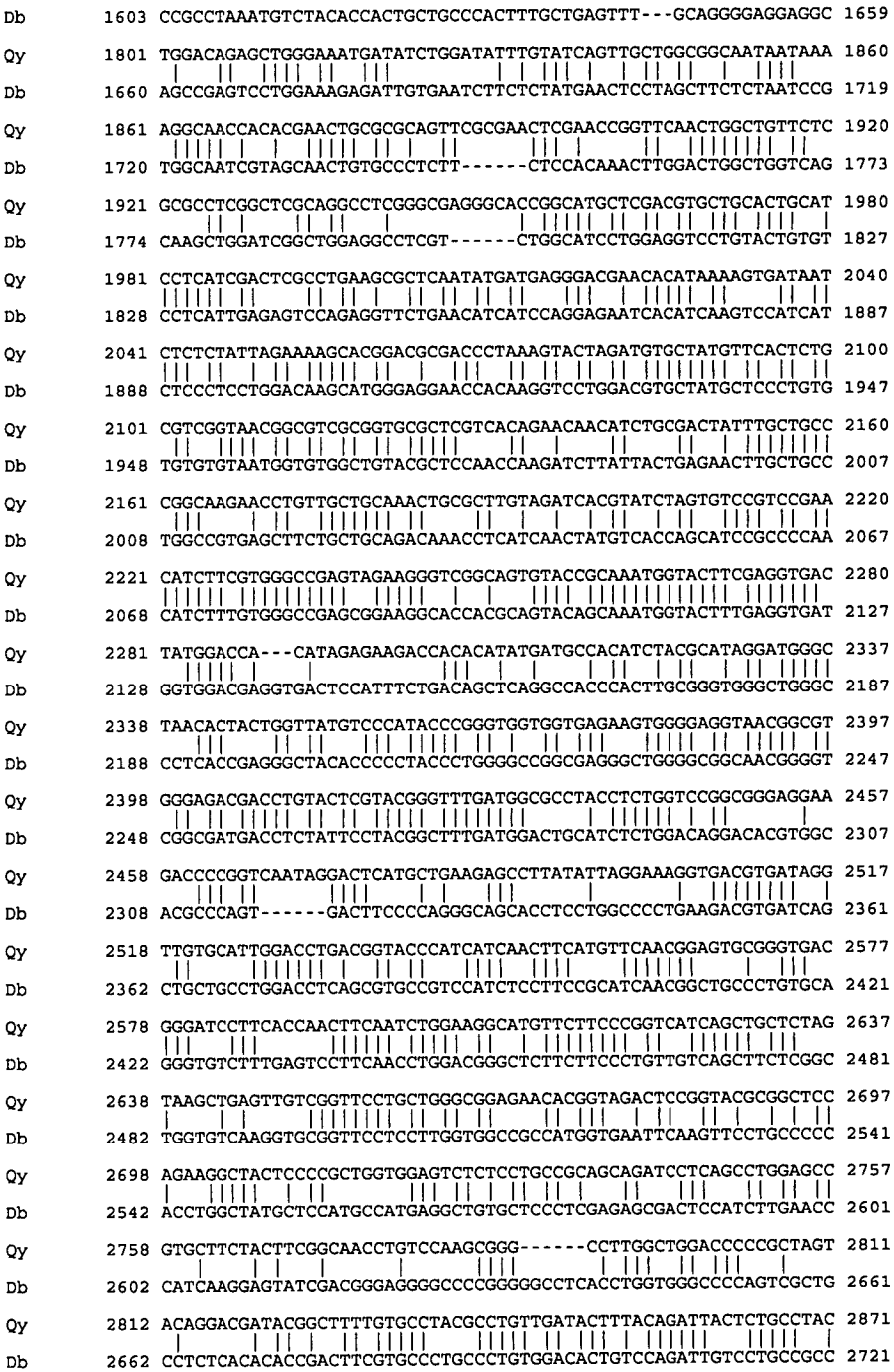


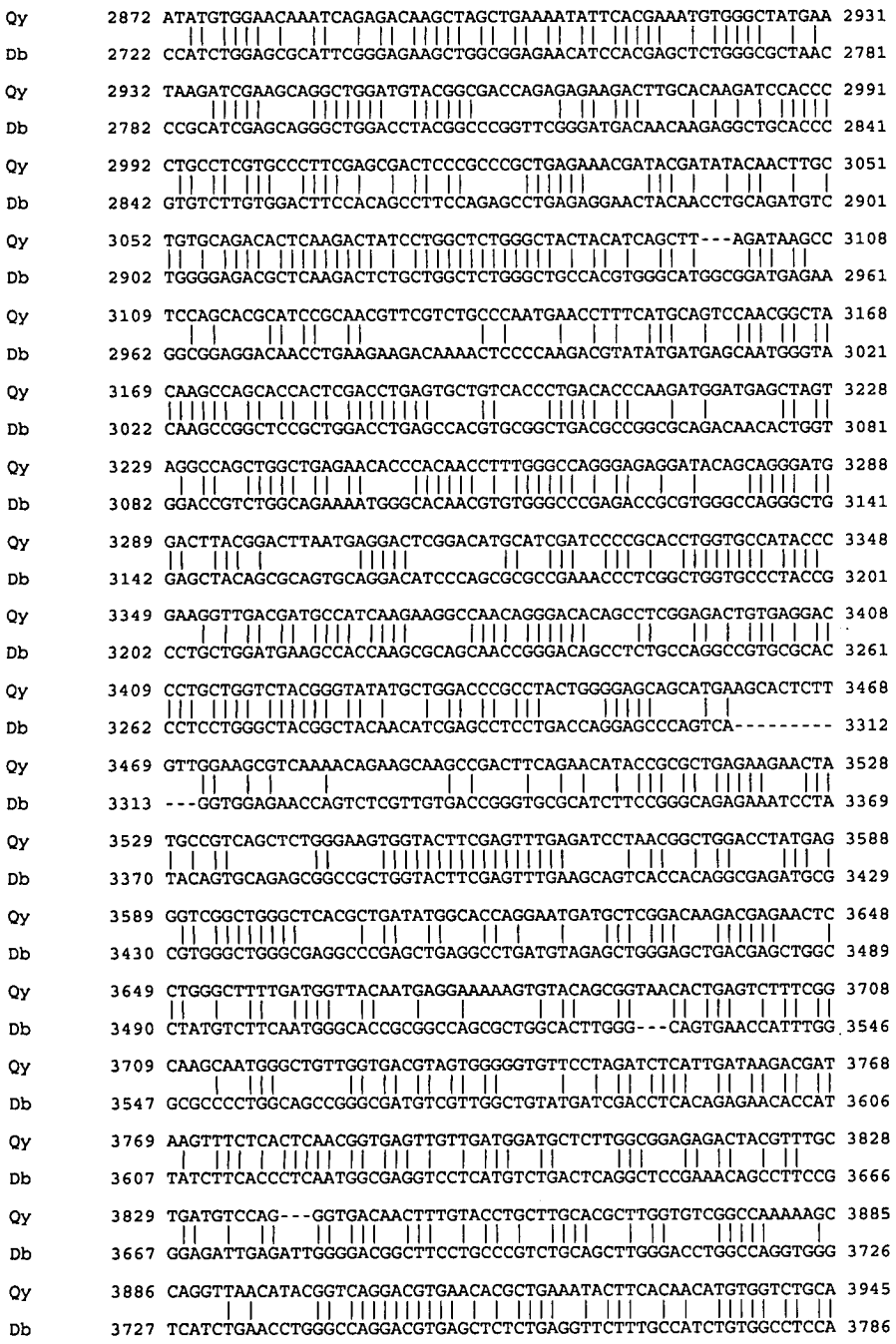


RESULT 15
US-10-276-774-500
; Sequence 500, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 500
; LENGTH: 15359
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-500

Query Match 16.6%; Score 831.4; DB 8; Length 15359;
Best Local Similarity 54.8%; Pred. No. 5.9e-257;
Matches 2083; Conservative 0; Mismatches 1611; Indels 105; Gaps 18;







Search completed: October 10, 2006, 16:48:33
Job time : 3842 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: October 10, 2006, 15:44:20 ; Search time 1549 Seconds
(without alignments)
6000.794 Million cell updates/sec

Title: US-10-668-767-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 ctaaattcgaaattcccatc.....ggtgaccacccagtaccact 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2386913 seqs, 929522941 residues

Total number of hits satisfying chosen parameters: 4773826

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

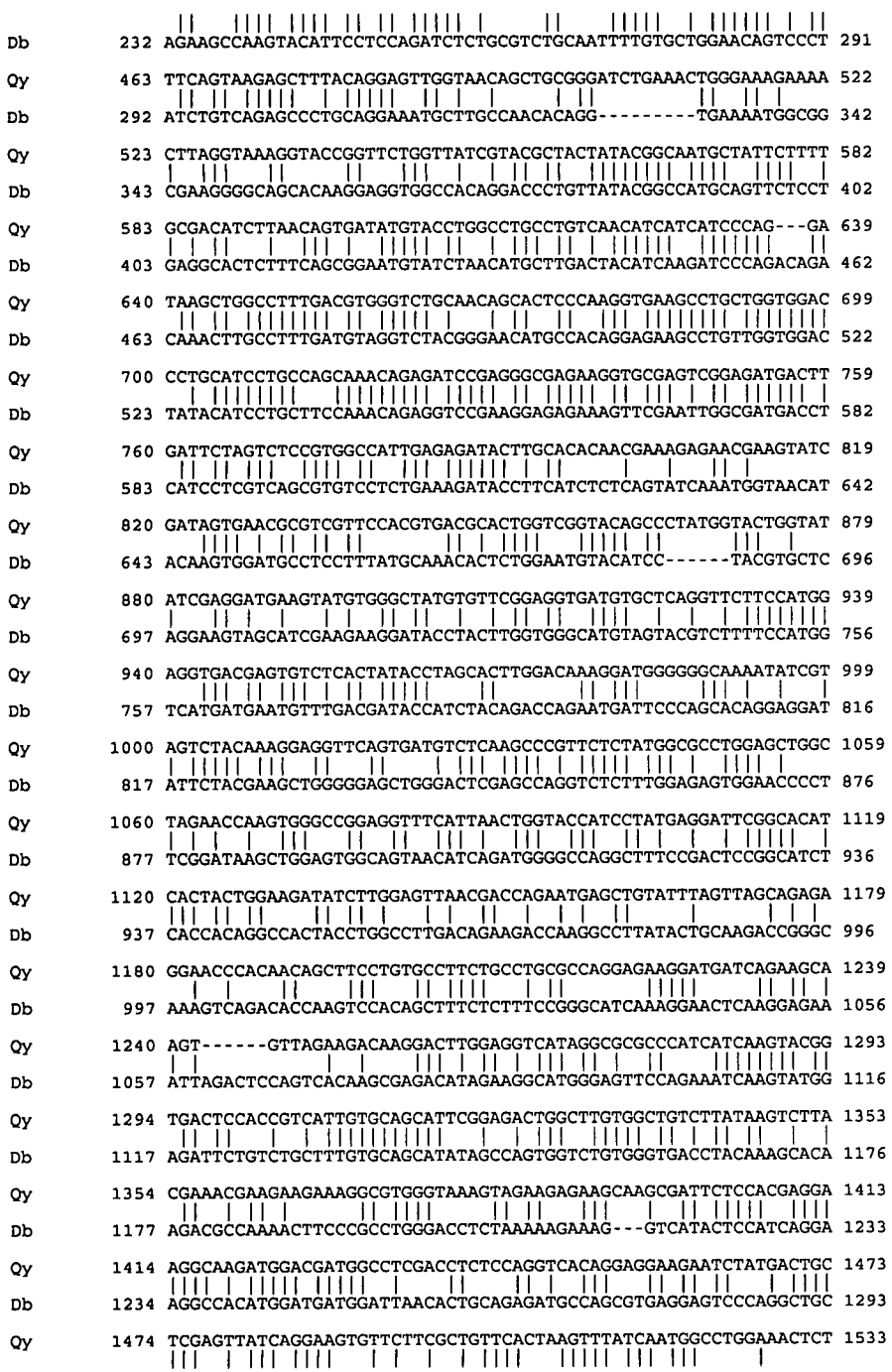
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	821.4	16.4	15563	8	US-11-266-748A-57467	Sequence 57467, A
	2	63	1.3	1406	8	US-11-266-748A-31954	Sequence 31954, A
c	3	54.8	1.1	583	8	US-11-266-748A-377158	Sequence 377158,
	4	54.8	1.1	583	8	US-11-266-748A-460537	Sequence 460537,
	5	43.4	0.9	349	8	US-11-266-748A-373619	Sequence 373619,
c	6	43.4	0.9	349	8	US-11-266-748A-456998	Sequence 456998,
c	7	42	0.8	84428	8	US-11-330-363-1	Sequence 1, Appli
	8	39.6	0.8	838	9	US-11-056-355B-14642	Sequence 14642, A
	9	39.6	0.8	4017	9	US-11-218-305-1911	Sequence 1911, Ap
	10	39.2	0.8	1189	9	US-11-174-307B-4053	Sequence 4053, Ap
	11	39.2	0.8	2294	9	US-11-218-305-4140	Sequence 4140, Ap
	12	39	0.8	895	9	US-11-218-305-12749	Sequence 12749, A
	13	39	0.8	1739	9	US-11-174-307B-3341	Sequence 3341, Ap
	14	39	0.8	1847	9	US-11-218-305-12750	Sequence 12750, A
	15	38.8	0.8	604	7	US-11-292-078-9801	Sequence 9801, Ap
	16	38.8	0.8	1841	9	US-11-218-305-11691	Sequence 11691, A
	17	37.8	0.8	2240	9	US-11-218-305-12186	Sequence 12186, A
	18	37.6	0.8	850	9	US-11-218-305-814	Sequence 814, App
	19	37.6	0.8	2167	6	US-10-449-902-65	Sequence 65, Appl
	20	37.6	0.8	2252	6	US-10-449-902-22166	Sequence 22166, A
	21	37.6	0.8	2300	6	US-10-449-902-20087	Sequence 20087, A
c	22	37.2	0.7	1420	9	US-11-218-305-14899	Sequence 14899, A
c	23	37.2	0.7	1613	9	US-11-218-305-14900	Sequence 14900, A
c	24	37.2	0.7	4106	9	US-11-218-305-14898	Sequence 14898, A
	25	37.2	0.7	4791	9	US-11-218-305-9027	Sequence 9027, Ap
c	26	37.2	0.7	129811	8	US-11-266-748A-59921	Sequence 59921, A
	27	37.2	0.7	201523	8	US-11-266-748A-29050	Sequence 29050, A
	28	37.2	0.7	4647455	6	US-10-641-321-205	Sequence 205, App
	29	37	0.7	1573	9	US-11-056-355B-62140	Sequence 62140, A
c	30	37	0.7	1990	6	US-10-449-902-13608	Sequence 13608, A
	31	37	0.7	2369	9	US-11-218-305-13345	Sequence 13345, A
	32	37	0.7	3193	6	US-10-449-902-6829	Sequence 6829, Ap
	33	37	0.7	3486	6	US-10-449-902-26867	Sequence 26867, A
	34	36.8	0.7	1071	6	US-10-449-902-15561	Sequence 15561, A
c	35	36.4	0.7	223	8	US-11-266-748A-230400	Sequence 230400,
	36	36.4	0.7	960	6	US-10-449-902-3368	Sequence 3368, Ap
	37	36.4	0.7	1015	6	US-10-449-902-2861	Sequence 2861, Ap
	38	36.4	0.7	1046	6	US-10-449-902-26606	Sequence 26606, A
	39	36.4	0.7	1612	6	US-10-449-902-9903	Sequence 9903, Ap
	40	36.4	0.7	2055	9	US-11-218-305-12179	Sequence 12179, A
	41	36.4	0.7	4376	8	US-11-266-748A-23511	Sequence 23511, A
	42	36.4	0.7	8726	8	US-11-266-748A-30587	Sequence 30587, A
	43	36.4	0.7	109559	6	US-10-539-228-137	Sequence 137, App
	44	36.2	0.7	1116	9	US-11-218-305-422	Sequence 422, App
	45	36.2	0.7	1514	9	US-11-218-305-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-11-266-748A-57467
; Sequence 57467, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57467
; LENGTH: 15563
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-57467

Query Match 16.4%; Score 821.4; DB 8; Length 15563;
Best Local Similarity 54.6%; Pred. No. 2.8e-243;
Matches 2082; Conservative 0; Mismatches 1631; Indels 102; Gaps 18;

```
Qy      346 GAGGGTGTGCCTGGCTGCCGAAGGTCTCGGCAACCGGCACTGCTTCCTGGAGAATATTGC 405
            || | | |||||||| ||||| || || || || || | |||||| ||||    | | |
Db      172 GAAGTTCTGCCTGGCAGCCGAGGGACTTGGGAATCGCCTGTGCTTCTTGGAACCCACTTC 231

Qy      406 CGA---CAAGAACATACCGCCTGATCTGTCGCAGTGTGTGTTTGTCATCGAACAGGCGCT 462
```


Db 232 AGAAGCCAAGTACATTCCTCCAGATCTCTGCGTCTGCAATTTTGTGCTGGAACAGTCCCT 291
Qy 463 TTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAAACTGGGAAAGAAAA 522
Db 292 ATCTGTCAGAGCCCTGCAGGAAATGCTTGCCAACACAGG---------TGAAAATGGCGG 342
Qy 523 CTTAGGTAAAGGTACCGGTTCTGGTTATCGTACGCTACTATACGGCAATGCTATTCTTTT 582
Db 343 CGAAGGGGCAGCACAAGGAGGTGGCCACAGGACCCTGTTATACGGCCATGCAGTTCTCCT 402
Qy 583 GCGACATCTTAACAGTGATATGTACCTGGCCTGCCTGTCAACATCATCATCCCAG---GA 639
Db 403 GAGGCACTCTTTCAGCGGAATGTATCTAACATGCTTGACTACATCAAGATCCCAGACAGA 462
Qy 640 TAAGCTGGCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAAGCCTGCTGGTGGAC 699
Db 463 CAAACTTGCCTTTGATGTAGGTCTACGGGAACATGCCACAGGAGAAGCCTGTTGGTGGAC 522
Qy 700 CCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCGAGAAGGTGCGAGTCGGAGATGACTT 759
Db 523 TATACATCCTGCTTCCAAACAGAGGTCCGAAGGAGAGAAAGTTCGAATTGGCGATGACCT 582
Qy 760 GATTCTAGTCTCCGTGGCCATTGAGAGATACTTGCACACAACGAAAGAGAACGAAGTATC 819
Db 583 CATCCTCGTCAGCGTGTCCTCTGAAAGATACCTTCATCTCTCAGTATCAAATGGTAACAT 642
Qy 820 GATAGTGAACGCGTCGTTCCACGTGACGCACTGGTCGGTACAGCCCTATGGTACTGGTAT 879
Db 643 ACAAGTGGATGCCTCCTTTATGCAAACACTCTGGAATGTACATCC------TACGTGCTC 696
Qy 880 ATCGAGGATGAAGTATGTGGGCTATGTGTTCGGAGGTGATGTGCTCAGGTTCTTCCATGG 939
Db 697 AGGAAGTAGCATCGAAGAAGGATACCTACTTGGTGGGCATGTAGTACGTCTTTTCCATGG 756
Qy 940 AGGTGACGAGTGTCTCACTATACCTAGCACTTGGACAAAGGATGGGGGGCAAAATATCGT 999
Db 757 TCATGATGAATGTTTGACGATACCATCTACAGACCAGAATGATTCCCAGCACAGGAGGAT 816
Qy 1000 AGTCTACAAAGGAGGTTCAGTGATGTCTCAAGCCCGTTCTCTATGGCGCCTGGAGCTGGC 1059
Db 817 ATTCTACGAAGCTGGGGGAGCTGGGACTCGAGCCAGGTCTCTTTGGAGAGTGGAACCCCT 876
Qy 1060 TAGAACCAAGTGGGCCGGAGGTTTCATTAACTGGTACCATCCTATGAGGATTCGGCACAT 1119
Db 877 TCGGATAAGCTGGAGTGGCAGTAACATCAGATGGGGCCAGGCTTTCCGACTCCGGCATCT 936
Qy 1120 CACTACTGGAAGATATCTTGGAGTTAACGACCAGAATGAGCTGTATTTAGTTAGCAGAGA 1179
Db 937 CACCACAGGCCACTACCTGGCCTTGACAGAAGACCAAGGCCTTATACTGCAAGACCGGGC 996
Qy 1180 GGAACCCACAACAGCTTCCTGTGCCTTCTGCCTGCGCCAGGAGAAGGATGATCAGAAGCA 1239
Db 997 AAAGTCAGACACCAAGTCCACAGCTTTCTCTTTCCGGGCATCAAAGGAACTCAAGGAGAA 1056
Qy 1240 AGT------GTTAGAAGACAAGGACTTGGAGGTCATAGGCGCGCCCATCATCAAGTACGG 1293
Db 1057 ATTAGACTCCAGTCACAAGCGAGACATAGAAGGCATGGGAGTTCCAGAAATCAAGTATGG 1116
Qy 1294 TGACTCCACCGTCATTGTGCAGCATTCGGAGACTGGCTTGTGGCTGTCTTATAAGTCTTA 1353
Db 1117 AGATTCTGTCTGCTTTGTGCAGCATATAGCCAGTGGTCTGTGGGTGACCTACAAAGCACA 1176
Qy 1354 CGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTCCACGAGGA 1413
Db 1177 AGACGCCAAAACTTCCCGCCTGGGACCTCTAAAAAGAAAG---GTCATACTCCATCAGGA 1233
Qy 1414 AGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGAGGAAGAATCTATGACTGC 1473
Db 1234 AGGCCACATGGATGATGGATTAACACTGCAGAGATGCCAGCGTGAGGAGTCCCAGGCTGC 1293
Qy 1474 TCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAATGGCCTGGAAACTCT 1533
Db 1294 TCGGATCATCCGGAACACTACAGCCTTATTCAGCCAGTTTGTCAGTGGAAACAA------ 1347
Qy 1534 TCAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACCTGGGCGAGATGGTGAT 1593
Db 1348 --------------TCGCACAGCTGCCCCCATCACCCTGCCTATAGAAGAAGTCCTGCA 1392
Qy 1594 GTGTCTTGAAGATCTCACCAACTACTTCGCACAGCCCGATGAGGATATGGAACACGAAGA 1653
Db 1393 GACCCTACAGGACTTGATCGCCTACTTCCAGCCCCCAGAGGAGGAGATGCGACATGAAGA 1452
Qy 1654 AAAGCAAAACAAATTCCGCGCCCTCCGCAACCGTCAGGACCTGTTCCAAGAGGAAGGCAT 1713
Db 1453 CAAGCAGAACAAGCTCCGCTCACTCAAAAACAGACAAAATCTTTTCAAGGAAGAGGGAAT 1512
Qy 1714 ACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCGTCACGTCCCAGGGGTTCCT 1773
Db 1513 GTTGGCCCTTGTCTTAAATTGCATTGACCGCTTAAATGTCTACAATAGCGTAGCACACTT 1572
Qy 1774 GGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCTGGATATTT 1833
Db 1573 TGCAGGGA---TTGCAAGGGAAGAGAGTGGCATGGCCTGGAAAGAAATTCTGAACCTCCT 1629
Qy 1834 GTATCAGTTGCTGGCGGCAATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAA 1893
Db 1630 CTACAAATTGCTGGCTGCTCTCATTCGCGGAAACAGAAACAATTGCGCTCAATT------ 1683
Qy 1894 CTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCAC 1953
Db 1684 CTCCAATAACCTTGATTGGCTCATCAGTAAATTGGACAGACTAGAATCTTCCT------C 1737
Qy 1954 CGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAAGCGCTCAATATGAT 2013
Db 1738 AGGTATCTTGGAAGTTTTGCACTGCATCTTAACTGAAAGCCCAGAAGCCTTAAATCTGAT 1797
Qy 2014 GAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCACGGACGCGACCCTAA 2073
Db 1798 AGCGGAGGGCCACATCAAGTCGATCATCTCCCTGTTGGATAAGCACGGGCGGAATCACAA 1857
Qy 2074 AGTACTAGATGTGCTATGTTCACTCTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACA 2133
Db 1858 GGTTCTGGATATCCTGTGCTCCCTCTGTCTCTGCAATGGGGTTGCAGTGAGAGCCAACCA 1917
Qy 2134 GAACAACATCTGCGACTATTTGCTGCCCGGCAAGAACCTGTTGCTGCAAACTGCGCTTGT 2193
Db 1918 GAATCTGATCTGTGACAACTTGCTGCCCCGGAGAAACCTACTCCTGCAGACACGACTGAT 1977
Qy 2194 AGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGCCGAGTAGAAGGGTCGGCAGT 2253
Db 1978 TAACGATGTAACCAGTATCCGGCCAAACATCTTCCTGGGAGTCGCGGAGGGCTCAGCCCA 2037
Qy 2254 GTACCGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGACC---ACACATAT 2310
Db 2038 GTACAAGAAGTGGTACTTCGAGCTGATTATCGACCAGGTGGACCCCTTCCTAACAGCAGA 2097
Qy 2311 GATGCCACATCTACGCATAGGATGGGCTAACACTACTGGTTATGTCCCATACCCGGGTGG 2370
Db 2098 GCCCACACATCTGCGGGTGGGCTGGGCCTCTTCTTCAGGCTATGCCCCATACCCAGGAGG 2157
Qy 2371 TGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGACGACCTGTACTCGTACGGGTTTGATGG 2430
Db 2158 TGGAGAAGGATGGGGAGGCAATGGTGTTGGTGACGACCTGTACTCCTATGGCTTTGATGG 2217
Qy 2431 CGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCGGTCAATAGGACTCATGCTGAAGAGCC 2490
Db 2218 ACTTCACCTTTGGTCAGGCCGGATACCCAGAGCTGT------GGCTTCCATCAACCAGCA 2271
Qy 2491 TTATATTAGGAAAGGTGACGTGATAGGTTGTGCATTGGACCTGACGGTACCCATCATCAA 2550
Db 2272 CCTCCTGAGATCGGATGACGTGGTAAGCTGCTGCCTGGACCTCGGGGTGCCCAGCATCTC 2331
Qy 2551 CTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAGGCAT 2610
Db 2332 ATTCCGCATCAATGGGCAGCCCGTGCAGGGGATGTTTGAGAACTTCAACACAGACGGGCT 2391

```
Qy       2611 GTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGA 2670
Db       2392 CTTCTTCCCTGTGATGAGCTTTTCAGCAGGTGTCAAAGTACGTTTCCTGATGGGTGGACG 2451

Qy       2671 ACACGGTAGACTCCGGTACGCGGCTCCAGAAGGCTACTCCCCGCTGGTGGAGTCTCTCCT 2730
Db       2452 TCATGGAGAGTTTAAGTTCCTGCCTCCCTCTGGCTATGCCCCTTGCTATGAAGCCTTACT 2511

Qy       2731 GCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGCAACCTGTC------CAA 2784
Db       2512 TCCAAAAGAGAAGATGAGATTGGAGCCTGTCAAAGAATATAAACGTGATGCTGATGGCAT 2571

Qy       2785 GCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACGGCTTTTGTGCCTACGCCTGT 2844
Db       2572 TAGAGATCTCTTGGGTACCACCCAGTTCCTCTCCCAAGCCTCTTTCATCCCATGCCCCGT 2631

Qy       2845 TGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATCAGAGACAAGCTAGCTGA 2904
Db       2632 AGACACCAGTCAGGTTATTTTGCCACCTCACCTAGAAAAGATCCGAGACAGACTAGCTGA 2691

Qy       2905 AAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACCA 2964
Db       2692 AAACATCCATGAGCTTTGGGGAATGAATAAAATAGAACTTGGCTGGACTTTCGGCAAGAT 2751

Qy       2965 GAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTTCGAGCGACTCCCGCCCGC 3024
Db       2752 ACGAGATGACAATAAAAGACAACACCCTTGCCTTGTGGAGTTTTCAAAGCTCCCAGAAAC 2811

Qy       3025 TGAGAAACGATACGATATACAACTTGCTGTGCAGACACTCAAGACTATCCTGGCTCTGGG 3084
Db       2812 TGAGAAGAACTATAACCTGCAAATGTCAACTGAAACCTTAAAAACCCTCTTGGCCCTGGG 2871

Qy       3085 CTACTACATCAGCTTAGATAAGC---CTCCAGCACGCATCCGCAACGTTCGTCTGCCCAA 3141
Db       2872 GTGCCACATTGCTCATGTTAACCCAGCTGCTGAGGAGGATCTCAAGAAGGTCAAACTGCC 2931

Qy       3142 TGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCAC 3201
Db       2932 CAAAAACTATATGATGTCCAACGGCTATAAGCCAGCCCCTTTGGATTTGTCTGATGTGAA 2991

Qy       3202 CCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTG 3261
Db       2992 GCTGTTACCTCCTCAAGAAATTTTAGTGGATAAGCTTGCAGAAAATGCACACAATGTTTG 3051

Qy       3262 GGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAATGAGGACTCGGACATGCA 3321
Db       3052 GGCAAAAGACAGAATAAAACAAGGATGGACCTATGGCATCCAACAGGATTTGAAGAACAA 3111

Qy       3322 TCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAG 3381
Db       3112 AAGAAATCCCCGTCTGGTGCCATATGCATTACTGGATGAGCGTACCAAGAAGTCAAACAG 3171

Qy       3382 GGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGGTATATGCTGGACCCGCC 3441
Db       3172 GGACAGCCTGCGGGAAGCTGTGCGCACTTTTGTTGGTTACGGGTATAACATTGAGCCATC 3231

Qy       3442 TACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAACAGAAGCAAGCCGACTT 3501
Db       3232 ---------AGACCAAGAACTAGCTGACTCGGCTGTGGAGAAGGTCAGCATAGACAAGAT 3282

Qy       3502 CAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAGTT 3561
Db       3283 CCGATTTTTCCGGGTAGAGCGATCTTATGCAGTGAGATCTGGAAAGTGGTATTTTGAGTT 3342

Qy       3562 TGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCAGG 3621
Db       3343 TGAAGTGGTGACTGGAGGAGACATGCGAGTCGGCTGGGCGAGGCCAGGCTGTCGACCTGA 3402

Qy       3622 AATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGATGGTTACAATGAGGAAAAAGT 3681
Db       3403 TGTCGAGCTGGGGGCCGATGACCAAGCCTTTGTGTTTGAAGGCAACAGGGGCCAGCGTTG 3462

Qy       3682 GTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGT 3741
Db       3463 GCATCAAGGAAG---TGGGTATTTTGGGCGTACCTGGCAGCCAGGGGATGTGGTCGGATG 3519

Qy       3742 GTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAACGGTGAGTTGTTGATGGA 3801
Db       3520 TATGATTAACCTGGATGATGCTTCAATGATCTTCACACTGAATGGGGAGCTGCTGATCAC 3579

Qy       3802 TGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAA---CTTTGTACCTGC 3858
Db       3580 CAACAAAGGCTCTGAACTTGCCTTCGCTGACTACGAGATTGAGAATGGCTTCGTGCCCAT 3639

Qy       3859 TTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAGGACGTGAACACGCT 3918
Db       3640 CTGCTGTCTGGGTCTATCTCAGATCGGCCGCATGAATCTCGGGACAGATGCCAGTACCTT 3699

Qy       3919 GAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTCTGTGTCAATATGAA 3978
Db       3700 CAAGTTTTATACCATGTGCGGTCTCCAAGAGGGCTTTGAGCCTTTTGCTGTCAACATGAA 3759

Qy       3979 GAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAGAATACGGATGAGAT 4038
Db       3760 CAGAGATGTTGCTATGTGGTTCAGCAAGCGCCTCCCGACGTTTGTCAA---CGTGCCAAA 3816

Qy       4039 GATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGATACACCTCCATGCCT 4098
Db       3817 GGATCATCCACACATAGAGGTCATGAGGATTGATGGCACCATGGACAGCCCTCCGTGTCT 3876

Qy       4099 CAAGATTTCCCACAACACGTTTGAGACGATGGAGA 4133
Db       3877 CAAGGTGACGCATAAGACATTTGGCACACAGAATA 3911
```

RESULT 2
US-11-266-748A-31954
; Sequence 31954, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31954
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31954

Query Match 1.3%; Score 63; DB 8; Length 1406;
Best Local Similarity 70.6%; Pred. No. 3.4e-08;
Matches 84; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```
Qy        675 CCCAAGGTGAAGCCTGCTGGTGGACCCTGCATCCTGCCAGCAAACAGAGATCCGAGGGCG 734
              ||  ||| || || ||||||||||||| |||| || |||  ||| ||||| || || || |
Db        789 CCATAGGAGAGGCTTGCTGGTGGACCATGCACCCAGCCTCCAAGCAGAGGTCTGAAGGAG 848

Qy        735 AGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATTGAGAGATACTTG 793
              | ||||| || || || |||||| | || || |||   ||  ||   ||| | ||| ||
Db        849 AAAAGGTCCGCGTTGGGGATGACATCATCCTTGTCAGTGTCTCCTCCGAGCGCTACCTG 907


RESULT 3
US-11-266-748A-377158/c
; Sequence 377158, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 377158
;   LENGTH: 583
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-377158

  Query Match             1.1%;  Score 54.8;  DB 8;  Length 583;
  Best Local Similarity   65.6%;  Pred. No. 6.8e-06;
  Matches   80;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy       3162 ACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATG 3221
              | ||||||| ||    || | |||||| |||||||| |||||| | |   || || | |
Db        455 AAGGCTACAACCCTCAGCCCCCCGACCTTAGTGCTGTTACCCTGTCCCGGGAGCTGCAGG 396

Qy       3222 AGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGC 3281
              | | ||  || ||||| || ||   |||||||   ||||   || ||| ||  |||
Db        395 CCATGGCAGAACAACTGGCAGAAAATTACCACAACACGTGGGGACGGAAGAAGAAGCAGG 336

Qy       3282 AG 3283
              ||
Db        335 AG 334


RESULT 4
US-11-266-748A-460537
; Sequence 460537, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 460537
;   LENGTH: 583
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-460537

  Query Match             1.1%;  Score 54.8;  DB 8;  Length 583;
  Best Local Similarity   65.6%;  Pred. No. 6.8e-06;
  Matches   80;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy       3162 ACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATG 3221
              | ||||||| ||    || | |||||| |||||||| |||||| | |   || || | |
Db        129 AAGGCTACAACCCTCAGCCCCCCGACCTTAGTGCTGTTACCCTGTCCCGGGAGCTGCAGG 188

Qy       3222 AGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGC 3281
              | | ||  || ||||| || ||   |||||||   ||||   || ||| ||  |||
Db        189 CCATGGCAGAACAACTGGCAGAAAATTACCACAACACGTGGGGACGGAAGAAGAAGCAGG 248

Qy       3282 AG 3283
              ||
Db        249 AG 250


RESULT 5
US-11-266-748A-373619
; Sequence 373619, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
```

```
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 373619
;   LENGTH: 349
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-373619

  Query Match             0.9%;  Score 43.4;  DB 8;  Length 349;
  Best Local Similarity   57.9%;  Pred. No. 0.017;
  Matches   77;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy       3151 CATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACC 3210
              ||  |||  |||| ||||||  || || || ||||||||        ||    ||  |
Db        148 CAACCAGGGCAACAGCTACAGTCCTGCTCCCCTCGACCTCTCAAACGTTGTGCTCTCCAG 207

Qy       3211 CAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGA 3270
               || |  | |   | || |      ||||||||||   |||||  | |||||| | |
Db        208 AGAGCTCCAGGGAATGGTGGAGGTCGTGGCTGAGAACTATCACAATATCTGGGCCAAGAA 267

Qy       3271 GAGGATACAGCAG 3283
              || ||  | | ||
Db        268 GAAGAAGCTGGAG 280


RESULT 6
US-11-266-748A-456998/c
; Sequence 456998, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 456998
;   LENGTH: 349
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-456998

  Query Match             0.9%;  Score 43.4;  DB 8;  Length 349;
  Best Local Similarity   57.9%;  Pred. No. 0.017;
  Matches   77;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy       3151 CATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACC 3210
              ||  |||  |||| ||||||  || || || ||||||||        ||    ||  |
Db        202 CAACCAGGGCAACAGCTACAGTCCTGCTCCCCTCGACCTCTCAAACGTTGTGCTCTCCAG 143

Qy       3211 CAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGA 3270
               || |  | |   | || |      ||||||||||   |||||  | |||||| | |
Db        142 AGAGCTCCAGGGAATGGTGGAGGTCGTGGCTGAGAACTATCACAATATCTGGGCCAAGAA 83

Qy       3271 GAGGATACAGCAG 3283
              || ||  | | ||
Db         82 GAAGAAGCTGGAG 70


RESULT 7
US-11-330-363-1/c
; Sequence 1, Application US/11330363
; Publication No. US20060121577A1
; GENERAL INFORMATION:
;  APPLICANT: Meiji Seika Kaisha, Ltd.
;  TITLE OF INVENTION: Midecamycin biosynthetic genes
;  FILE REFERENCE: 138451 US
;  CURRENT APPLICATION NUMBER: US/11/330,363
;  CURRENT FILING DATE:  2006-01-12
;  PRIOR APPLICATION NUMBER: US/10/229,148
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: 210516/2002
;  PRIOR FILING DATE: 2002-07-19
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 84428
;   TYPE: DNA
;   ORGANISM: Streptomyces mycarofaciens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((1)..(675))
;   OTHER INFORMATION: ORF42 (fragment)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((1168)..(2202))
;   OTHER INFORMATION: ORF41
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((2220)..(3215))
;   OTHER INFORMATION: ORF40
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((3237)..(4691))
;   OTHER INFORMATION: ORF39
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((4695)..(5948))
;   OTHER INFORMATION: ORF38
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((6048)..(6629))
;   OTHER INFORMATION: ORF37
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: Complement((6653)..(7945))
;   OTHER INFORMATION: ORF36
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8149)..(9015)
;   OTHER INFORMATION: ORF35
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9012)..(9335)
;   OTHER INFORMATION: ORF34
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9328)..(10458)
;   OTHER INFORMATION: ORF33
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10521)..(11603)
;   OTHER INFORMATION: ORF32
;   FEATURE:
;   NAME/KEY: CDS
```

; LOCATION: (11729)..(12961)
; OTHER INFORMATION: ORF31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((13016)..(14044))
; OTHER INFORMATION: ORF30
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((14074)..(15096))
; OTHER INFORMATION: ORF29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15643)..(17466)
; OTHER INFORMATION: ORF28
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((17522)..(18895))
; OTHER INFORMATION: ORF27
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19063)..(20229)
; OTHER INFORMATION: ORF26
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((20307)..(21743))
; OTHER INFORMATION: ORF25
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((21733)..(22527))
; OTHER INFORMATION: ORF24
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((22534)..(23571))
; OTHER INFORMATION: ORF23
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((23555)..(24463))
; OTHER INFORMATION: ORF22
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((24460)..(25650))
; OTHER INFORMATION: ORF21
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((25647)..(26105))
; OTHER INFORMATION: ORF20
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((26180)..(27391))
; OTHER INFORMATION: ORF19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27937)..(28983)
; OTHER INFORMATION: ORF18
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29244)..(42779)
; OTHER INFORMATION: ORF1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42823)..(48657)
; OTHER INFORMATION: ORF2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48712)..(59802)
; OTHER INFORMATION: ORF3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59850)..(64556)
; OTHER INFORMATION: ORF4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64687)..(70365)
; OTHER INFORMATION: ORF5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70365)..(71078)
; OTHER INFORMATION: ORF6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71113)..(72360)
; OTHER INFORMATION: ORF7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72400)..(73665)
; OTHER INFORMATION: ORF8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73694)..(75043)
; OTHER INFORMATION: ORF9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((75899)..(76570))
; OTHER INFORMATION: ORF10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((76602)..(77765))
; OTHER INFORMATION: ORF11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78039)..(79313)
; OTHER INFORMATION: ORF12
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((79391)..(81052))
; OTHER INFORMATION: ORF13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81541)..(82356)
; OTHER INFORMATION: ORF14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82760)..(83362)
; OTHER INFORMATION: ORF15
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((83495)..(84142))
; OTHER INFORMATION: ORF16
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84329)..(84428)
; OTHER INFORMATION: ORF17 (fragment)
US-11-330-363-1

Query Match 0.8%; Score 42; DB 8; Length 84428;
Best Local Similarity 54.5%; Pred. No. 1.8;
Matches 84; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```
Qy       1840 GTTGCTGGCGGCAATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAA 1899
              | || | ||||||    |     ||| |    ||| | || || ||| | |   | |||
Db      73362 GATGATCGCGGCACAGCTCGGCAGCAGCGCGTCGAGCGGCACGAAGTCCACCGGCACGAC 73303

Qy       1900 CCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCAT 1959
                ||      |||||     |||| || |||   |||| ||| | | || ||||  |
Db      73302 GTTGTCGGGAAGGCTGCCGAGGCGCTTCTGCTGCGAGGCATCGAGGGTGGCCACCACCTC 73243

Qy       1960 GCTCGACGTGCTGCACTGCATCCTCATCGACTCG 1993
              | ||  | ||| || | ||  |   | | |||||
Db      73242 GATCTCCATGCGGCCCAGCGCCTGAAGCAACTCG 73209
```

RESULT 8
US-11-056-355B-14642
; Sequence 14642, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

```
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 14642
;   LENGTH: 838
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(838)
;   OTHER INFORMATION: Ceres Seq. ID no. 12468112
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(838)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15225703
;   OTHER INFORMATION: as cited in SEQ ID NO 59527
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(838)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12615972
;   OTHER INFORMATION: as cited in SEQ ID NO 62455
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(838)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13596229
;   OTHER INFORMATION: as cited in SEQ ID NO 68800
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(838)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15179393
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-14642

  Query Match             0.8%;  Score 39.6;  DB 9;  Length 838;
  Best Local Similarity   49.5%;  Pred. No. 0.46;
  Matches  102;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy       2580 GATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTA 2639
             | ||| ||  || |  ||   | | || |||| |   || | |||||| |  | | |  |
Db        179 GGTCCATCTACACCAACAGATTTGCAGCCATGCTGAACCTGATCATCATCGCCGCCATCA 238

Qy       2640 AGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAG 2699
             | |||        || | || | |  ||  ||  ||       | |     || |    |
Db        239 ACCTGGCGCTCGGGATACTCCCGCACGTTGACAACTTCGCGCACATCGGCGGGTTCGCCA 298

Qy       2700 AAGGCTACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGT 2759
              ||||| |  ||     | | |   ||  | | ||  ||| ||    | |||||| |
Db        299 CAGGCTTCCTCCTCGGCTTCGTGCTGCTGATCCAGCCCCAGTTCGGGTGGCTGGAGCAGC 358

Qy       2760 GCTTCTACTTCGGCAACCTGTCCAAG 2785
              ||||     |   | |  |||||||
Db        359 CCTTCGGTGCCAAGACCAAGTCCAAG 384


RESULT 9
US-11-218-305-1911
; Sequence 1911, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1911
;   LENGTH: 4017
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-1911

  Query Match             0.8%;  Score 39.6;  DB 9;  Length 4017;
  Best Local Similarity   49.5%;  Pred. No. 1.3;
  Matches  102;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy       2580 GATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTA 2639
             | ||| ||  || |  ||   | | || |||| |   || | |||||| |  | | |  |
Db       3340 GGTCCATCTACACCAACAGATTTGCAGCCATGCTGAACCTGATCATCATCGCCGCCATCA 3399

Qy       2640 AGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAG 2699
             | |||        || | || | |  ||  ||  ||       | |     || |    |
Db       3400 ACCTGGCGCTCGGGATACTCCCGCACGTTGACAACTTCGCGCACATCGGCGGGTTCGCCA 3459

Qy       2700 AAGGCTACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGT 2759
              ||||| |  ||     | | |   ||  | | ||  ||| ||    | |||||| |
Db       3460 CAGGCTTCCTCCTCGGCTTCGTGCTGCTGATCCAGCCCCAGTTCGGGTGGCTGGAGCAGC 3519

Qy       2760 GCTTCTACTTCGGCAACCTGTCCAAG 2785
              ||||     |   | |  |||||||
Db       3520 CCTTCGGTGCCAAGACCAAGTCCAAG 3545


RESULT 10
US-11-174-307B-4053
; Sequence 4053, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4053
;   LENGTH: 1189
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1189)
;   OTHER INFORMATION: Ceres cDNA ID no. 21666056
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1189)
;   OTHER INFORMATION: Ceres CLONE  ID no. 1277411
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1189)
;   OTHER INFORMATION: Also known as  Ceres CDNA ID no. 24358413
US-11-174-307B-4053

  Query Match             0.8%;  Score 39.2;  DB 9;  Length 1189;
  Best Local Similarity   56.1%;  Pred. No. 0.77;
  Matches   74;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;
```

```
Qy       1880 GCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCC 1939
              | || ||||||   |  |  |  || ||   |     | ||||| ||  ||  || ||||
Db        863 GGGCTGTTCGCCGTCGTGGCCGTGTCCATGCGCAGCGTGTCGCGGCTGCGCCGGCGGGCC 922

Qy       1940 TCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAA 1999
               || ||| ||| ||| |  |||   ||  ||  ||||  ||||| ||| |  ||
Db        923 GGGGACGACGGCGCCGTCGCGCTGCTCGGCCTCAACTGGTTCCTCCTCGGCCTGCTCACC 982

Qy       2000 GCGCTCAATATG 2011
              ||| ||   ||
Db        983 TCGCCCATGCTG 994


RESULT 11
US-11-218-305-4140
; Sequence 4140, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4140
;   LENGTH: 2294
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(18)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-4140

  Query Match             0.8%;  Score 39.2;  DB 9;  Length 2294;
  Best Local Similarity   56.1%;  Pred. No. 1.2;
  Matches   74;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy       1880 GCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCC 1939
              | || ||||||   |  |  |  || ||   |     | ||||| ||  ||  || ||||
Db        245 GGGCTGTTCGCCGTCGTGGCCGTGTCCATGCGCAGCGTGTCGCGGCTGCGCCGGCGGGCC 304

Qy       1940 TCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCCTGAA 1999
               || ||| ||| ||| |  |||   ||  ||  ||||  ||||| ||| |  ||
Db        305 GGGGACGACGGCGCCGTCGCGCTGCTCGGCCTCAACTGGTTCCTCCTCGGCCTGCTCACC 364

Qy       2000 GCGCTCAATATG 2011
              ||| ||   ||
Db        365 TCGCCCATGCTG 376


RESULT 12
US-11-218-305-12749
; Sequence 12749, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12749
;   LENGTH: 895
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-12749

  Query Match             0.8%;  Score 39;  DB 9;  Length 895;
  Best Local Similarity   54.5%;  Pred. No. 0.74;
  Matches   78;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       1853 ATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGG 1912
              || |   | | |  | | |  |    | ||||| ||| || |     | |  ||| |
Db        296 ATGAAGCAGGACCTCAAGATCACGGACACGCAGATCGAGATCCTCGCCGGCATCATCAAT 355

Qy       1913 CTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTG 1972
              | | ||||| | |||||||||  ||  |||||  |    ||| |  ||||| |  || |
Db        356 ATCTACTCGCTCGTCGGCTCGCTCGCGGCGGGCCGGACGTCCGACTGGCTCGGCCGGCGG 415

Qy       1973 CACTGCATCCTCATCGACTCGCC 1995
              ||  |||  |  |||   || |
Db        416 TACACCATGGTGCTCGCGGCGGC 438


RESULT 13
US-11-174-307B-3341
; Sequence 3341, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3341
;   LENGTH: 1739
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1739)
;   OTHER INFORMATION: Ceres cDNA ID no. 21572848
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1739)
;   OTHER INFORMATION: Ceres CLONE  ID no. 1532145
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1739)
;   OTHER INFORMATION: Also known as  Ceres CDNA ID no. 24359342
US-11-174-307B-3341

  Query Match             0.8%;  Score 39;  DB 9;  Length 1739;
  Best Local Similarity   54.5%;  Pred. No. 1.2;
  Matches   78;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       1853 ATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGG 1912
              || |   | | |  | | |  |    | ||||| ||| || |     | |  ||| |
Db        243 ATGAAGCAGGACCTCAAGATCACGGACACGCAGATCGAGATCCTCGCCGGCATCATCAAT 302

Qy       1913 CTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTG 1972
```

```
                | | |||||| | |||||||||  ||  |||||  |    ||| |  |||||  |  || |
Db        303 ATCTACTCGCTCGTCGGCTCGCTCGCGGCGGGCCGGACGTCCGACTGGCTCGGCCGGCGG 362

Qy       1973 CACTGCATCCTCATCGACTCGCC 1995
              ||  |||  |  |||   || |
Db        363 TACACCATGGTGCTCGCGGCGGC 385


RESULT 14
US-11-218-305-12750
; Sequence 12750, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12750
;   LENGTH: 1847
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-12750

  Query Match             0.8%;  Score 39;  DB 9;  Length 1847;
  Best Local Similarity   54.5%;  Pred. No. 1.2;
  Matches   78;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       1853 ATAATAAAAGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGG 1912
              || |   | | |  | | |  |    | ||||| ||| || |     | |  ||| |
Db        228 ATGAAGCAGGACCTCAAGATCACGGACACGCAGATCGAGATCCTCGCCGGCATCATCAAT 287

Qy       1913 CTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTG 1972
              | | |||||  | |||||||||  ||  |||||  |    ||| |  |||||  |  || |
Db        288 ATCTACTCGCTCGTCGGCTCGCTCGCGGCGGGCCGGACGTCCGACTGGCTCGGCCGGCGG 347

Qy       1973 CACTGCATCCTCATCGACTCGCC 1995
              ||  |||  |  |||   || |
Db        348 TACACCATGGTGCTCGCGGCGGC 370


RESULT 15
US-11-292-078-9801
; Sequence 9801, Application US/11292078
; Publication No. US20060195941A1
; GENERAL INFORMATION:
;  APPLICANT: Deikman, Jill
;  APPLICANT:  Feng, Paul C.C.
;  APPLICANT:  Fincher, Karen L.
;  APPLICANT:  Ziegler, Todd E.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.346 - 38-21(52274)C
;  CURRENT APPLICATION NUMBER: US/11/292,078
;  CURRENT FILING DATE:  2005-12-02
;  PRIOR APPLICATION NUMBER: US 10/021,323
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,619
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 9801
;   LENGTH: 604
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(604)
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB3828-028-Q6-K6-C7
US-11-292-078-9801

  Query Match             0.8%;  Score 38.8;  DB 7;  Length 604;
  Best Local Similarity   58.8%;  Pred. No. 0.65;
  Matches   67;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy       1346 AAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTC 1405
              |||| | |  | |  ||      | |    ||||||||| |||||| || | | | |||
Db        369 AAGTTTGAAAAGAGCAAACTAGAGGAGAAGGGTAAAGTTGAAGAGCAGGATGTGCTTCAG 428

Qy       1406 CACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCCAGGTCACAGGAGGAA 1459
              |   || | |  ||| |  |  | | ||||||  | || |||  | | ||||||
Db        429 CTTAAGAAGGAGAAGGTTCAGAAAGACCTCGAGATTTCTAGGCTAAAAGAGGAA 482


Search completed: October 11, 2006, 02:43:59
Job time : 1555 secs
```